

Result No.	Query			ID	Description
	Score	Match	Length		
1	230.5	12.6	237	2	T52432
2	201	11.0	383	2	P96582
3	138.5	7.6	115	2	B96664
4	138.5	7.6	618	2	S68450
5	137.5	7.5	604	2	S68449
6	136.5	7.5	316	2	T32659
7	134.5	7.3	428	2	T48167
8	131.5	7.2	358	2	JC5964
9	130	7.1	943	2	S68824
10	124.5	6.8	200	2	A96664
11	123	6.7	275	2	A45679
12	121.5	6.6	124	2	T01251
13	118	6.4	286	2	D36828
14	118	6.4	292	2	T41772
15	117.5	6.4	824	2	T16028
16	116.5	6.4	268	2	T10304
17	116.5	6.4	268	2	A53989
18	116.5	6.4	299	2	T45881
19	116	6.3	433	2	JC7678
20	115.5	6.3	739	2	E86434
21	115	6.3	497	2	S69545
22	112.5	6.1	288	2	D97113
23	112.5	6.1	522	2	T18504
24	112	6.1	275	2	T10310
25	112	6.1	496	2	S68452
26	111	6.1	401	2	G96824
27	110.5	6.0	337	2	T48341
28	110	6.0	754	2	S35503
29	110	6.0	797	2	AH1674

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: UNIPROT:Q9SYH3; GB:AE005173; NID:94587558; PIDN:AAD25789.1; GSPDB:GN
C:Genetics:
A:Gene: FLS11.25
A:Map position: 1

Query Match 11.0%; Score 201; DB 2; Length 383;
Best Local Similarity 21.5%; Pred. No. 1.5e-07;
Matches 81; Conservative 71; Mismatches 171; Indels 54; Gaps 13;

Qy 14 LLGTTSVTAALYSV-YRQARVSQELKGAKKVHGLGDLKSLSEAPGKCPV-----64
Db 23 ILGTLAVSAVGSALKYASTNAALKTKDAPEVSI-SDLRSLLPASEDKSETNDRKNSD 81
Qy 65 --YAVIEGAVRSVETLNSQVENCCKGVIQRLTLQEHKVMWNRTHLWNCDSKIIHOR-- 120
Db 82 QRIVVRGVVK--PKISDEGKNNVLISPETGDKALIIQRTQTVYVSGMKELFQSTGH 139
Qy 121 -----TNTVPFDLPVHEDGVD---VAVRV---LKPLDSVDLGLTVEYKFP 159
Db 140 RFMLERSLRKHGADFTRTVPFVGVKQSQNSSFVAVNMGSRQPLP-----LTTVYNR 194
Qy 160 HPSIQSFDTDVICHVISGRPKGIQETHEMLKVGATLTCVGLVDNNSVRLQPPKQMGY 219
Db 195 QPINSSFLQA---FLYPDYPVGLLDIEKILPPGDKDITAVG-IYFNNGVPEIKSCQDLFY 250
Qy 220 YLSSQDFDLQROESSVRLMKVALVFGFATCATLFFILRKQYLQRLRLKQOMQEEF 279
Db 251 FLSEMTDKMIEDLMEQTNFVLGSLVILGIVSGILSYAAVRTW---NKKWQNHQREL 306
Qy 280 QEHEAQLLSRAKPEDRESLSKA--CVVCLSFKSCVFLGCHVCSCTCYRALPEP--KK 335
Db 307 PQRPNDSVVDDEPEDADEIPDGELCVICVSRRRVPAPFCGHVWCRCRCSTVERELNPK 366
Qy 336 CPICRQAITRVIPLNS 352
Db 367 CPVCLQISGRSMRVYS 383

RESULT 3
B96664
probable RING zinc finger protein T12P18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96664
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <STO>

A:Cross-references: UNIPROT:Q9CAK3; GB:AE005173; NID:g6358794; PIDN:AAF07375.1; GSPDB:GN
C:Genetics:
A:Gene: T12P18.8
A:Map position: 1

Query Match 7.6%; Score 138.5; DB 2; Length 115;
Best Local Similarity 30.2%; Pred. No. 0.0016;
Matches 35; Conservative 19; Mismatches 46; Indels 17; Gaps 4;

Qy 248 GFATCATLFFILR---KQYLQRLRLKQOMQEEFQHEAQLLSRAKPEDRESLSKA--- 301
Db 2 GF-TVLGVFLITKHVIDSVLERRRRLQKRVLDAAAKRAELESESGNSGTRESLSDSTKK 60
Qy 302 -----CVVCLSFKSCVFLGCHVCSCTCYRALPEPCKPCICRQAITRVIPLY 350
Db 61 EDVAVDLCVLCRQEQYNAVFPVCGHMCCTACSSHL---TSCPLCRRRIDLAVKTY 113

RESULT 4
S68450
apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <L1S>
A:Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:gl184317; PIDN:AAC50372.1; PID:gl1 C:Function:
C:Keywords: apoptosis; zinc finger
P:567-611/Domain: RING finger homology <RNG>

Query Match 7.6%; Score 138.5; DB 2; Length 618;
Best Local Similarity 21.5%; Pred. No. 0.014;
Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;

Qy 82 QFVENCCKGVIQRLTLQEHKVMWNRTHLWNCDSKIIHRTNTVPFDLPVHEDGVDAVRV 141
Db 343 EFVDEIQRYPHLL--EQLLSTSDTTGSENADPPIIH-----FGGSSSSSDAVMM 391
Qy 142 LKPL--DSVDLGL-----ETVYKFPHSIQSF---TDVIGHYISGERPKIQE---TE 186
Db 392 NTPVVKSALEMGFNRLVKQTVLSKILTTGENYKTVNDIVSALLNAEDEKREEKEKQAE 451
Qy 187 EMLKVGATLTGVGL-----VLDN-----NSVRLQPP---KQGMQYVLSQD-PD 227
Db 452 EMASDDLIRKRNWALFQQLTCVLPILDNLKANVINKQEHDDIHKQTIQIPLOARELID 511
Qy 228 SLLQRESSVRLMKVALVFGFATCATLFFILRKQYLQOE-----RLRLKQOMQEEFOE 281
Db 512 TIWKGNAANIFKNCKLEIDSTLYKNLFDVKMVKYIPTEDVSGLSLEQLRLQOE--- 568
Qy 282 HEAQLLSRAKPEDRESLSKACVCLSSFKSCVFLGCHVCSCTCYRALPEPCKPCICRQ 341
Db 569 -----RTCKVCMDKEVSVVVFPCGHLWVQCRC---APSLURKPCPICRG 607
Qy 342 AITRVIPLNS 352
Db 608 ILKGTVRIFLS 618

RESULT 5
S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449


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Db      121 S-RVHVMGARGATGALTVGSEVFEESSCSRLVRGTLDYQLQKMLGVKRIERVLPITGIPL 179
QY      196 TVGUGEL 201
      |
      |||:
Db      180 TIVGEV 185

RESULT 11
A45679
Inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C;Species: Cydia pomonella granulosis virus CpGV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: UNIPROT:P41436; GB:I05494; NID:G289583; PIDN:AAA43835.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match      6.7%; Score 123; DB 2; Length 275.

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A;Molecule type: DNA
A;Residues: 1-824 <TAI>
A;Cross-references: EMBL:U40945; NID:g1072208; PID:g1072213; PIDN:AAA81723.1; CESP:F10D7
C;Genetics:
A;Gene: CESP:F10D7.5
A;introns: 83/1; 108/1; 136/2; 174/1; 217/1; 236/2; 278/2; 325/3; 354/3; 384/1; 399/3; 4
C;Superfamily: fruit fly inger protein neuralized; RING finger homology
F;769-817/Domain: RING finger homology <RRN>

Query Match 6.4%; Score 117.5; DB 2; Length 824;
Best Local Similarity 34.7%; Pred. No. 0.77;
Matches 26; Conservative 7; Mismatches 35; Indels 7; Gaps 2;

Qy 279 FQHEAQLLSRAKPEDRESILKSAVCVCLSSFKSCVFLCQGHVCSCTECYALPEPK-KCP 337
Db 756 FQNEGNGAQEVNEGDE-----CTICMDAPVNSVLYTCGHMCMCFECGRLLTTKGTCP 809

Qy 338 ICRQAITRVIPLVNS 352
Db 810 ICRAPVDVITKYS 824

Search completed: November 6, 2004, 17:39:02
Job time : 42 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 20:11:02 ; Search time 9629 Seconds
(without alignments)
11570.727 Million cell updates/sec

Title: US-09-978-360A-32
Perfect score: 2356
Sequence: 1 atccttggcgccacagtcgg.....aaccaaaaaaaaaaaaaa 2356

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_rn.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	100.0	2356	6	AR306576
2	2356	100.0	2356	6	AX061650
3	2356	100.0	2374	9	BC014010
4	2345	99.5	2382	9	BC010101
5	2338.4	99.3	2413	6	AX191590
6	2336.8	99.2	2401	6	BD170650
7	2335.2	99.1	2401	6	BD170649
8	2335.2	99.1	2401	9	AB097015
9	2332	99.0	2442	6	AX879967
10	2332	99.0	2442	6	BD158122
11	2332	99.0	2442	9	AK022937
12	2330.8	98.9	2431	6	AX428888
13	2291.8	97.3	2717	6	AX405813
14	2217	94.1	2377	6	AX274867
15	1973.4	83.8	195076	9	AL391357
16	1951.4	82.8	126141	2	AL356300
17	1768.2	75.1	163801	2	AC025224
18	1059	44.9	1059	6	AX191580
19	862	36.6	972	6	CQ727201

20	846.6	35.9	1354	10	BC019516
21	589	25.0	259224	2	AC109006
22	584.2	24.8	170878	2	AC107845
23	584.2	24.8	248479	10	AL807249
24	479.6	20.4	1143	5	BC068869
25	476.6	20.2	512	6	AX873089
26	476.6	20.2	512	6	BD153151
27	363	15.4	374	6	AX333839
28	338.8	14.4	484	6	AX868018
29	338.8	14.4	484	6	BD148080
30	309	13.1	343	6	BD077897
31	307.4	13.0	378	6	BD076018
32	304.6	12.9	391	6	BD076940
33	298.2	12.7	184991	2	BX927120
34	294.2	12.5	476	11	G26878
35	200.6	8.5	201	11	BV199951
36	195.2	8.3	260	6	CQ659938
37	162.4	6.9	175	6	CQ657979
38	146.6	6.2	162087	5	BX649599
39	142.2	6.0	2674	5	BC059797
40	124.6	5.3	197	6	BD075982
41	113.4	4.8	2748	5	BC079729
42	95.6	4.1	1086	6	CQ572652
43	95.6	4.1	1243	3	AX113263
44	74.6	3.2	3475	6	CQ572651
45	74.6	3.2	45258	2	AC015395

ALIGNMENTS

RESULT 1	AR306576	2356 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	Sequence 55 from patent US 6548633.				
DEFINITION	Sequence 55 from patent US 6548633.				
ACCESSION	AR306576				
VERSION	AR306576.1	GI:31696645			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2356)				
AUTHORS	Edwards, J.-B. D.M., Bougueret, L. and Jobert, S.				
TITLE	Complementary DNA's encoding proteins with signal peptides				
JOURNAL	Patent: US 6548633-A 55 15-APR-2003;				
FEATURES	Location/Qualifiers				
source	1..2356				
	/organism="unknown"				
	/mol_type="genomic DNA"				

ORIGIN

Query Match	100.0%;	Score 2356;	DB 6;	Length 2356;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATCCTTGGCGCCACAGTCGCGCCACCGGGGCTCGCCGCGCTCATGGAGAGCGGAGGGCGGC	60	
Db	1	ATCCTTGGCGCCACAGTCGCGCCACCGGGGCTCGCCGCGCTCATGGAGAGCGGAGGGCGGC	60	
QY	61	CCTCGTGTGCCAGTTTCATCTCTGGGACCACTCTGTGTGTACCGCGCCCTGTACT	120	
Db	61	CCTCGTGTGCCAGTTTCATCTCTGGGACCACTCTGTGTGTACCGCGCCCTGTACT	120	
QY	121	CCGTGTACCGGAGAGCGCGGGTCTCCAGAGCTCAAGGAGCTAAGGAGCTAAGGAGCTAAT	180	
Db	121	CCGTGTACCGGAGAGCGCGGGTCTCCAGAGCTCAAGGAGCTAAGGAGCTAAGGAGCTAAT	180	
QY	181	TGGGTGAAGATTAAAGAGTATCTTTCAGAGCTCCAGGAAATCCGTCCTTATGCTG	240	
Db	181	TGGGTGAAGATTAAAGAGTATCTTTCAGAGCTCCAGGAAATCCGTCCTTATGCTG	240	
QY	241	TTATAGAGGAGCTGTGGGTCTGTTAAAGAAACGCTTAACAGCCAGTTTGGGAAACT	300	

Fri Nov 12 12:23:27 2004

Db	241	TTATAGAGGAGCTGTGGGTCTGTTTAAAGAACGCTTAACAGCCAGTTTGTGGAAAACT	300
Qy	301	GCAGGGGTAAATTCAGGGCTGACACTTCAGAGACACAGATGTTGGAAATCGAACCA	360
Db	301	GCAGGGGTAAATTCAGGGCTGACACTTCAGAGACACAGATGTTGGAAATCGAACCA	360
Qy	361	CCACCTTTGGATGATGCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG	420
Db	361	CCACCTTTGGATGATGCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG	420
Qy	421	ACCTGGTGCCTCCACAGGATGGGTGATGTTGCTGTGCGAGTCTGAAGCCCTGCACT	480
Db	421	ACCTGGTGCCTCCACAGGATGGGTGATGTTGCTGTGCGAGTCTGAAGCCCTGCACT	480
Qy	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAAGTTCCACCCCTCGATTCACTTCA	540
Db	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAAGTTCCACCCCTCGATTCACTTCA	540
Qy	541	CCGATGTCATCGCCACTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600
Db	541	CCGATGTCATCGCCACTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600
Qy	601	AGATGCTGAAGGTGGGGCCACCTTCACAGGGTTGGGAACTGGTCTGTGACACAACT	660
Db	601	AGATGCTGAAGGTGGGGCCACCTTCACAGGGTTGGGAACTGGTCTGTGACACAACT	660
Qy	661	CTGTCGGCTGAGCGGCCCAACAGCATGCACTATCTTAAGCAGCCAGGACTTTCG	720
Db	661	CTGTCGGCTGAGCGGCCCAACAGCATGCACTATCTTAAGCAGCCAGGACTTTCG	720
Qy	721	ACAGCTCTGTCAGAGGAGGAGTCTGAGCTCAGGCTCTGGAAGTGTGCGCTGGTTT	780
Db	721	ACAGCTCTGTCAGAGGAGGAGTCTGAGCTCAGGCTCTGGAAGTGTGCGCTGGTTT	780
Qy	781	TTGGCTTTGCCACATGTGCCACCTCTTCAATCTCCGGAAGCGTATCTGACGCGC	840
Db	781	TTGGCTTTGCCACATGTGCCACCTCTTCAATCTCCGGAAGCGTATCTGACGCGC	840
Qy	841	AGAGGCTCTGGCTCAGACGATCAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC	900
Db	841	AGAGGCTCTGGCTCAGACGATCAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC	900
Qy	901	TGAGCGAGCAAGCTCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGATGTGTCTGA	960
Db	901	TGAGCGAGCAAGCTCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGATGTGTCTGA	960
Qy	961	GCAGCTTCAAGTCTCTGCTTCTGAGTGTGGGACAGTTTGTCTGACCGAGTCT	1020
Db	961	GCAGCTTCAAGTCTCTGCTTCTGAGTGTGGGACAGTTTGTCTGACCGAGTCT	1020
Qy	1021	ACCGGCTCTGAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCGGGTGA	1080
Db	1021	ACCGGCTCTGAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCGGGTGA	1080
Qy	1081	TACCCCTGTCAACAGCTAATAGTTTGAAGCCGACAGCTGTGCTGGAAGCACCCCTG	1140
Db	1081	TACCCCTGTCAACAGCTAATAGTTTGAAGCCGACAGCTGTGCTGGAAGCACCCCTG	1140
Qy	1141	CCCCCTTTTCAAGGATTTTATCTGAGGCTTTTGAAGGACAGTGTGGGGTAGCTGT	1200
Db	1141	CCCCCTTTTCAAGGATTTTATCTGAGGCTTTTGAAGGACAGTGTGGGGTAGCTGT	1200
Qy	1201	CACCTCCAGGTATGATGAGGAGGAAATGGGTAGAACTCTCCAGACCCAATGCTCCAA	1260
Db	1201	CACCTCCAGGTATGATGAGGAGGAAATGGGTAGAACTCTCCAGACCCAATGCTCCAA	1260
Qy	1261	TGGCAGGATGCTGCTTTCCACCTGAGAGGAGCCCTGTCTCATGTGAGGCTCATAGA	1320
Db	1261	TGGCAGGATGCTGCTTTCCACCTGAGAGGAGCCCTGTCTCATGTGAGGCTCATAGA	1320
Qy	1321	GCCTCACCTGGAGGATGCTGCTTTCCAGGAGCCAGATCAGTGCAGTGTG	1380
Db	1321	GCCTCACCTGGAGGATGCTGCTTTCCAGGAGCCAGATCAGTGCAGTGTG	1380
Qy	1381	ACTGAAATGCCTCATCATCTTAAGCACCAAGCCAGTATCAGACGCTCTTCTGTTCCCTG	1440
Db	1381	ACTGAAATGCCTCATCATCTTAAGCACCAAGCCAGTATCAGACGCTCTTCTGTTCCCTG	1440
Qy	1441	TGCTCTCTGTTTTTTTCTGTTGAATCGTTGCTGCTGTGAGTCTGTTGGAGGACTCAGAG	1500
Db	1441	TGCTCTCTGTTTTTTTCTGTTGAATCGTTGCTGCTGTGAGTCTGTTGGAGGACTCAGAG	1500
Qy	1501	GGAGGAAAGGCTGGGCCCCGAGTACAAACGATGCTTGGTGTGCTCCGCAAGAGACT	1560
Db	1501	GGAGGAAAGGCTGGGCCCCGAGTACAAACGATGCTTGGTGTGCTCCGCAAGAGACT	1560
Qy	1561	CTGCGCAGCTTTCTTTCTTTTCTCATGCCCCGGGAAACAGTCTTTCTCAGAAATGT	1620
Db	1561	CTGCGCAGCTTTCTTTCTTTTCTCATGCCCCGGGAAACAGTCTTTCTCAGAAATGT	1620
Qy	1621	CAGCTGGGAGGCTCAACTTGTGTTCTTCTTCCCTCAGCTGCTTGCCTTAAACGCTG	1680
Db	1621	CAGCTGGGAGGCTCAACTTGTGTTCTTCTTCCCTCAGCTGCTTGCCTTAAACGCTG	1680
Qy	1681	CACGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGACATCCGCTTCTGCCAGATGTT	1740
Db	1681	CACGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGACATCCGCTTCTGCCAGATGTT	1740
Qy	1741	CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTTGGTCAGGAGGCC	1800
Db	1741	CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTTGGTCAGGAGGCC	1800
Qy	1801	TCCTGGTTTCGCCACTGGCCCTGATTTGAACTCTGCGCACCTGGAGAGCTCGGGGTGT	1860
Db	1801	TCCTGGTTTCGCCACTGGCCCTGATTTGAACTCTGCGCACCTGGAGAGCTCGGGGTGT	1860
Qy	1861	CCCTGGTTTCCCTCTGAGAGATGAGCGCAGAGGCTCGCTCTCTGAAGACACGAGT	1920
Db	1861	CCCTGGTTTCCCTCTGAGAGATGAGCGCAGAGGCTCGCTCTCTGAAGACACGAGT	1920
Qy	1921	TGAGTGCCACTGCGCTAGTGTCTGCGCTCAGAGCTTCTTCAAGGCTGTCAAGGAA	1980
Db	1921	TGAGTGCCACTGCGCTAGTGTCTGCGCTCAGAGCTTCTTCAAGGCTGTCAAGGAA	1980
Qy	1981	AAGCAGCGGCTGGGCAACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCGCTG	2040
Db	1981	AAGCAGCGGCTGGGCAACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCGCTG	2040
Qy	2041	CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTTGTGTACCCCTCCAGTATT	2100
Db	2041	CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTTGTGTACCCCTCCAGTATT	2100
Qy	2101	ACCATTTGCCCTCACTGCGCTTGGTGTAGCCCTTTTAGTCAAGACAGATGGGGCTGTTT	2160
Db	2101	ACCATTTGCCCTCACTGCGCTTGGTGTAGCCCTTTTAGTCAAGACAGATGGGGCTGTTT	2160
Qy	2161	TCGCCACCTCTCAGTAGTTGGAGTCAATACACAGCTCTTTTATTTATTTGCTTTCT	2220
Db	2161	TCGCCACCTCTCAGTAGTTGGAGTCAATACACAGCTCTTTTATTTATTTGCTTTCT	2220
Qy	2221	GCCTCTGAATTTTCACTCTCTGCTCTCTTGTGAGGAGGAGGAGGAGGAGGAGGAGG	2280
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DEFINITION Sequence 55 from Patent WO0100806.
ACCESSION AX061650
VERSION AX061650.1 GI:12406759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS dumas milne Edwards,J.B., Bougueleret,L. and Jobert,S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 55 04-JAN-2001;
GENSET (FR)
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.C., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, V.S., Krzyzinski, G.I., Skalski, U., Smalhus, D.E., Schnerch, A., Schein, J.F., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

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Strausberg, R.

Direct Submission
Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk
Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granites, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrifop, S., Thomas, P.J., Touchman, J.W., Tsurgan, C., Vogt, J.H., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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DB	1644	CAGGCTGGGCAAGGTCAACTTGTTGTTTCTTTTCCCTTCACCTGTGCTCTCTTAAACGCCCTG	1703
QY	1681	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGCATCCGCTTCTGCCCCAGATGTT	1740
DB	1704	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGCATCCGCTTCTGCCCCAGATGTT	1763
QY	1741	CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTGGTCAAGCAGGCC	1800
DB	1764	CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTGGTCAAGCAGGCC	1823
QY	1801	TCCTGGTTTCGCCACTCGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGGGGTGTT	1860
DB	1824	TCCTGGTTTCGCCACTCGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGGGGTGTT	1883
QY	1861	CCCTGGTTTTCCCTCTGGAGAAATGAGCGCGAGAGGCTCGCCTCTCTGAAAGCAGCAGTG	1920
DB	1884	CCCTGGTTTTCCCTCTGGAGAAATGAGCGCGAGAGGCTCGCCTCTCTGAAAGCAGCAGTG	1943
QY	1921	TGATGCCACTGGCCCTAGTGTCTCTGGCCTCACAGCTTCCCTTGCAAGGCTGTCAAGGAA	1980
DB	1944	TGATGCCACTGGCCCTAGTGTCTCTGGCCTCACAGCTTCCCTTGCAAGGCTGTCAAGGAA	2003
QY	1981	AAGCAGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGGCCGCTCG	2040
DB	2004	AAGCAGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGGCCGCTCG	2063
QY	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCGCTTCTCCTTGTTTACCCCTCCCGAGTATT	2100
DB	2064	CAGCTTTGACATCTTGGTGTACTCATGTGCGCTTCTCCTTGTTTACCCCTCCCGAGTATT	2123
QY	2101	ACCAATTTGCCCTCACCTGCGCCTTGGTGAGCCCTTTAGTCSAAGACAGATGGGCGCTTTT	2160
DB	2124	ACCAATTTGCCCTCACCTGCGCCTTGGTGAGCCCTTTAGTCSAAGACAGATGGGCGCTTTT	2183
QY	2161	TCCCCCACTCTGAGTGTGAGGTCACATACACAGCTC-TTTTTTTTATTGCCCCCTTTC	2219
DB	2184	TCCCCCACTCTGAGTGTGAGGTCACATACACAGCTCTTTTTTTATTGCCCCCTTTC	2243
QY	2220	TGSCCTCTGAATGTTTCATCTCTCGTCTCTTTGTGAGCGAGGAAAGGGTGCCTCAGG	2279
DB	2244	TGSCCTCTGAATGTTTCATCTCTCGTCTCTTTGTGAGCGAGGAAAGGGTGCCTCAGG	2303
QY	2280	GGCCGACACTAGTATGATGTCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC	2339
DB	2304	GGCCGACACTAGTATGATGTCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC	2363
QY	2340	CAAAAAAAAAAAAAA	2356
DB	2364	CAAAAAAAAAAAAAA	2380

RESULT 5
AX191590
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

AX191590 2413 bp DNA linear PAT 15-AUG-2001
Sequence 112 from Patent WO0149728.
AX191590
AX191590.1 GI:15209773
Homo sapiens (human)

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Kato, S. and Kimura, T.
TITLE	Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL	Patent: WO 0149728-A 112 12-JUL-2001;
FEATURES	Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
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ORIGIN	
	Query Match 99.3%; Score 2338.4; DB 6; Length 2413;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 2339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 ATCTCTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGCTCATGGAGCGAGGGCGGC 60
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QY	61 CCTCGTGTGCCAGTTATCTCTCTGGCACCACTCTGTGGTCAACCGCGCCCTGTACT 120
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QY	121 CCGTGATCCGCGAGAGCCCGGGTCTCCCAAGAGCTCAAGGAGCTAAAAAGTTCA 180
Db	194 CCGTGATCCGCGAGAGCCCGGGTCTCCCAAGAGCTCAAGGAGCTAAAAAGTTCA 253
QY	181 TGGGTGAAGATTAAAGAGTATCTTTCAGAAGCTTCCAGGAAATGGTGCTTATGCTG 240
Db	254 TGGGTGAAGATTAAAGAGTATCTTTCAGAAGCTTCCAGGAAATGGTGCTTATGCTG 313
QY	241 TTATAGAGAGAGCTGTGGGTCTGTTAAAGAAACGCTTAAAGAGTTCGGAAGAACT 300
Db	314 TTATAGAGAGAGCTGTGGGTCTGTTAAAGAAACGCTTAAAGAGTTCGGAAGAACT 373
QY	301 GCAAGGGGTAAATTCAGCGGCTGACACTTCAGGAGCAACAAGATGGTGGGAATCGAACCA 360
Db	374 GCAAGGGGTAAATTCAGCGGCTGACACTTCAGGAGCAACAAGATGGTGGGAATCGAACCA 433
QY	361 CCACCTTTGGAATGATTTGCTCAAAAGATCATTTATCAGAGGACCAACACAGTGCCTTTG 420
Db	434 CCACCTTTGGAATGATTTGCTCAAAAGATCATTTATCAGAGGACCAACACAGTGCCTTTG 493
QY	421 ACCTGTGCCCCACAGAGATGGCGTGGATGTGGCTGTGGAGTGTGAAGCCCTTGGACT 480
Db	494 ACCTGTGCCCCACAGAGATGGCGTGGATGTGGCTGTGGAGTGTGAAGCCCTTGGACT 553
QY	481 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA 540
Db	554 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA 613
QY	541 CCGATGTCATCGGCCACTACATCAGCGGCTGAGCGGCCCAAGAGCATCCAAAGAGACCGAGG 600
Db	614 CCGATGTCATCGGCCACTACATCAGCGGCTGAGCGGCCCAAGAGCATCCAAAGAGACCGAGG 673
QY	601 AGATGCTGAAGGTGGGGGCCACCCCTCACAGGGGTGGCGAATGTGCTCTGGACCAACAAT 660

DB	1982	TGGATGCCACTGGCCTAGTGTCTCTGGGCTCACAGCTTCTCTGCAAGGCTGTCAACAGGAA	2040
QY	1981	AAGAGCGGCTGGCACCCTGACATATGCCCTCTTGGGCTCCCTCATCCAGCCCGCTCG	2040
DB	2042	AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGCTCG	2101
QY	2041	CAGCTTTGACATCTTTGGTGTACTCATGTGCTTCTCCCTTGTGTACCCCTCCCAATTT	2100
DB	2102	CAGCTTTGACATCTTTGGTGTACTCATGTGCTTCTCCCTTGTGTACCCCTCCCAATTT	2161
QY	2101	ACCATTTGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTCAACAGATGGGGCTGTTT	2160
DB	2162	ACCATTTGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTCAACAGATGGGGCTGTTT	2221
QY	2161	TCCCCCACTCTAGTAGTGTGGAGGTACATACACAGCTCTTTTATTTGCCCTTTTCT	2280
DB	2222	TCCCCCACTCTAGTAGTGTGGAGGTACATACACAGCTCTTTTATTTGCCCTTTTCT	2281
QY	2221	GCCTCTGAATGTTTCATCTCTCGTCTCTCTCTTGTGAGGAGGAGGGGTGCCCTCAGG	2280
DB	2282	GCCTCTGAATGTTTCATCTCTCGTCTCTCTCTTGTGAGGAGGAGGGGTGCCCTCAGG	2344
QY	2281	GCCGACACTAGTATGATGCACTGTCAGGTGCCAGTGTGAACAGAGAAATTAACATGTTGCAACC	2344
DB	2342	GCCGACACTAGTGTGATGCACTGTCAGGTGCCAGTGTGAACAGAGAAATTAACATGTTGCAACC	2403
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LOCUS	BD170649	2401 bp	DNA linear PAT 17-JAN-2002
DEFINITION	NF-kappa B activation gene.		
ACCESSION	BD170649		
VERSION	BD170649.1	GI:27876461	
KEYWORDS	WO 02053737-A/37.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Matsuda, A., Honda, G., Muramatsu, S. and Nagano, Y.		
TITLE	NF-kappa B activation gene		
JOURNAL	Patent: WO 02053737-A 37 11-JUL-2002;		
COMMENT	ASAH KASEI CORP, AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO		
	OS Homo sapiens (human)		
	PN WO 02053737-A/37		
	PD 11-JUL-2002		
	PF 25-DEC-2001 WO 2001JP011389		
	PR 28-DEC-2000 JP 00P 402288, 26-MAR-2001 JP 01P 088912 PR		
	24-AUG-2001 JP 01P 254018		
	PI AKIO MATSUDA, GOICHI HONDA, SHUJI MURAMATSU, YUKIKO NAGANO PC		
	C12N1/12, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/PC		
	10,		
	PC		
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	A61P35/00, C12Q1/68, C12N9/00, G01N33/15, G01N33/50, G01N33/53, PC		
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	CC NF-kappa B activation gene		
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Best Local Similarity	99.9%;	Pred. No. 0;	
Matches 2337; Conservative	0;	Mismatches 3;	Indels 0; Gaps

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Db
QY 61 CCTCGCTGTGCCAGTTCATCCTCCTGGGACACCTCTGTGGTCAACCGCCGCTGTACT 120
Db
QY 122 CCTCGCTGTGCCAGTTCATCCTCCTGGGACACCTCTGTGGTCAACCGCCGCTGTACT 181
QY 121 CCGTGTAACGGGAGAGGCCCGGGTCTCCCAAGAGTCAAGGGAGCTTAAAGAGTTCATT 180
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QY 181 TGGGTGAAGATTTAAAGAGTATTTCTTCAAGAGTCCAGGAAATCGTGCTTATGCTG 240
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Db 1142 TACCCCTGTACACAGCTAATAGTTTGAAGCGGCAACAGCTTGACCTTGAAGCACCCCTG 1201
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QY 2101 ACCATTGCCCCCTCACCTGCCCTTGGTGAAGCTTTTGTAGTGAAGAGATGGGCTGT 2160
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[illegible]

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Qy	2281	CGCGACACTAGTATGATGTCAGTGTCCAGTGTCAACAGCAGCAATTAACAATGTTGCAACC	2340
Db	2342	CGCGACACTAGTGTGATGTCAGTGTCCAGTGTCAACAGCAGCAATTAACAATGTTGCAACC	2401

RESULT	9
AX879967	
LOCUS	AX879967
DEFINITION	Sequence 14872 from Patent EP074617.
ACCESSION	AX879967
VERSION	AX879967.1
KEYWORDS	GI:40034703
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE	Primers for synthesising full-length cDNA and their use
JOURNAL	Patent: EP 1074617-A 14872 of 7-FEB-2001; Research Association for Biotechnology (JP)
FEATURES	Location/Qualifiers
source	1..2442
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CDS	

Query Match	99.0%;	Score 2332;	DB 6;	Length 2442;
Best Local Similarity	99.8%;	Pred. No. 0;		
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QY	1	ATCCTTGGCGCCACAGTCGGGCTCGCGGGGTTCGCGCGGCTCATGGAGAGCGGAGGCGGC	60	
Db	103	ATCCTTGGCGCCACAGTCGGGCTCGCGGGGTTCGCGCGGCTCATGGAGAGCGGAGGCGGC	165	
QY	61	CCTCGCTGTGGCAGTTTCATCTCTCTGGCACCACTCTGTGTGTACCGCGCCCTGTACT	120	
Db	163	CCTCGCTGTGCCAGTTTCATCTCTCTGGCACCACTCTGTGTGTACCGCGCCCTGTACT	222	
QY	121	CCGTGTACCGGCGAGAGGCCGGGTCTCCAAAGAGCTCAAGGAGCTTAAAAAGTTCAATT	180	
Db	223	CCGTGTACCGGCGAGAGGCCGGGTCTCCAAAGAGCTCAAGGAGCTTAAAAAGTTCAATT	282	
QY	181	TGGGTCAAGATTTAAAGAGTATCTTTTCAGAGCTCCAGGAAATCGGTGCCTTATGCTG	240	
Db	283	TGGGTCAAGATTTAAAGAGTATCTTTTCAGAGCTCCAGGAAATCGGTGCCTTATGCTG	342	
QY	241	TTATAGAAGGAGCTGTGCGGCTCTGTTTAAAGAAACGTTTAAACAGCCAGTTTGTGGAAAAC	300	
Db	343	TTATAGAAGGAGCTGTGCGGCTCTGTTTAAAGAAACGTTTAAACAGCCAGTTTGTGGAAAAC	402	
QY	301	GCAGGGGTAAATTCAGCGGCTGACATTTCAGGAGCACAAAGATGGTGTGGAATCGAACCA	360	
Db	403	GCAAGGGGTAAATTCAGCGGCTGACATTTCAGGAGCACAAAGATGGTGTGGAATCGAACCA	462	
QY	361	CCACCTTTTGGAAATGATGCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTTG	420	

TITLE	Primer for synthesizing full-length cDNA and use thereof
JOURNAL	Patent: JP 2002191363-A 12965 09-JUL-2002;
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/12965 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (144)..(1199).
FEATURES	Location/Qualifiers
source	1..2442
ORIGIN	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
Query Match	99.0%; Score 2332; DB 6; Length 2442;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 2335; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	1 ATCTTGGCGCACAGTGGCCACCGGGCTCGCGCGTCTGATGAGAGCGAGCGCGC 60
DB	103 ATCTTGGCGCACAGTGGCCACCGGGCTCGCGCGTCTGATGAGAGCGAGCGCGC 162
QY	61 CCTCGCTGGCAGTTTCACTCTCTGGGACACACCTCTGTGTACCGCGCGCTGTACT 120
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QY	121 CCGTGTACCGGAGAGCGCGGCTCTCCAGAGCTCAAGGAGCTCAAAAAGTTCAAT 180
DB	223 CCGTGTACCGGAGAGCGCGGCTCTCCAGAGCTCAAGGAGCTCAAAAAGTTCAAT 282
QY	181 TGGGTGAAGATTTAAAGATGATTTCTTCAAGCTCCAGGAAATGCGTCTATGCTG 240
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RESULT 12
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DEFINITION Sequence 9 from Patent WO0123538.
ACCESSION AX428888
VERSION AX428888.1 GI:21540280
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Hodgson,D.M., Lincoln,S.E., Russo,F.D., Spiro,P.A., Banville,S.C.,
Bratcher, Shawn.R., Dufour, Gerard,E., Cohen,H.J., Rosen,B.H.,
Shah,P., Chalup,M.S., Hillman,J.L., Jones, Anissa,L., Yu,J.Y.,
Greenawalt,L.B., Panzer,S.R., Roseberry,A.M., Wright, Rachel,J.,
Chen,W., Liu,T.F., Yap,P.E., Stockdreher,T.K., Amshey,S. and
Fong,W.T.
TITLE Molecules for disease detection and treatment
JOURNAL Patent: WO 0123538-A 9 05-APR-2001;
Incyte Genomics, Inc. (US)
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1921	QY	TGGATGCCACTGGCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980
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SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C.,	
JOURNAL		Azinai, Y., Bandman, O., Tang, Y.T., Mathur, P., Shah, P., Au-Young, J.	
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Fri Nov 12 12:23:27 2004

Db 2365 CAAAAA 2377

AL391357/c

LOCUS

DEFINITION

Human DNA sequence from clone RP11-401M16 on chromosome 1, complete sequence.

AL391357

AL391357.20 GI:16501137

HTG.

SOURCE

Homosapiens (human)

ORGANISM

Homosapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 195076)

Kimberley, A.

Direct Submission

Submitted (25-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

On Oct 26, 2001 this sequence version replaced gi:16304938.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr1

RP11-401M16 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-401M16 The true left end of clone RP11-72P17 is at 108464 in this sequence. The true right end of clone RP4-749H3 is at 12964 in this sequence.

FEATURES

source

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Job time : 9641 secs

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DB	901	TGAGCCGAGCCAAAGCTTGAGGACAGGAGTCTGAAGCGCTGTGTAGTGTCTCA	960
QY	961	GCAGCTTCAAGTCTGCGTCTTTCTGAGTGTGGGACGTTTCTCTCCACCGAGTGT	1020
DB	961	GCAGCTTCAAGTCTGCGTCTTTCTGAGTGTGGGACGTTTCTCTCCACCGAGTGT	1020
QY	1021	ACCGGCGCTTGCAGAGCCCAAGAGTGCCTATCTGAGACAGGGCGATCACCGGCTGA	1080
DB	1021	ACCGGCGCTTGCAGAGCCCAAGAGTGCCTATCTGAGACAGGGCGATCACCGGCTGA	1080
QY	1081	TACCCCTGTACACAGCTAATAGTTTGAAGCGCGACAGCTTCACTGGAAGCACCCCTG	1140
DB	1081	TACCCCTGTACACAGCTAATAGTTTGAAGCGCGACAGCTTCACTGGAAGCACCCCTG	1140
QY	1141	CCCCCTTTTCAGGATTTTATCTCGAGGCTTTTGGAGGACAGTGTGGGGTAGCTGT	1200
DB	1141	CCCCCTTTTCAGGATTTTATCTCGAGGCTTTTGGAGGACAGTGTGGGGTAGCTGT	1200
QY	1201	CACCTCCAGGTATGATTGAGGGAGGAATTTGGTAGAACTCTCCAGACCATGCTCTCAA	1260

Db	1201		CACCTCCAGGATGATGATTGAGGGAGGAATGGGTAGAACTCTCCAGACCCATGCCTCCAA	1260
Qy	1261		TGGCAGGATGCTGCCTTTCCCACTCAGAGGGGACCTCTCCATGTGCAGCCTCATCAGA	1320
Db	1261		TGGCAGGATGCTGCCTTTCCCACTCAGAGGGGACCTCTCCATGTGCAGCCTCATCAGA	1320
Qy	1321		GCCTCACCTGGGAGGATGCCGTGGCGTCTCTCCAGAGCCAGATCAGTGGCAGTGTG	1380
Db	1321		GCCTCACCTGGGAGGATGCCGTGGCGTCTCTCCAGAGCCAGATCAGTGGCAGTGTG	1380
Qy	1381		ACTGAAATGCTCATCATTTAAGCACCAAGCCAGTGATCAGCAGCTCTCTGTTCCTG	1440
Db	1381		ACTGAAATGCTCATCATTTAAGCACCAAGCCAGTGATCAGCAGCTCTCTGTTCCTG	1440
Qy	1441		TGCTCTCTGTTTTTCTCGTGAATCGTTGCTTGCTGTGGACATGTGGAGGACTCAGAG	1500
Db	1441		TGCTCTCTGTTTTTCTCGTGAATCGTTGCTTGCTGTGGACATGTGGAGGACTCAGAG	1500
Qy	1501		GGGAGAAAGGCTGGGCCCCGAGTCAACCGATGCCCTTGGGTGCTGCCTCCGAAGAGACT	1560
Db	1501		GGGAGAAAGGCTGGGCCCCGAGTCAACCGATGCCCTTGGGTGCTGCCTCCGAAGAGACT	1560
Qy	1561		CTGCCGAGCTTTTCTTTTTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
Db	1561		CTGCCGAGCTTTTCTTTTTCCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
Qy	1621		CAGCTGGGCAAGTCAACTGTCTTCTTTCCCTCACTGCTTGCCTCTCTTAAACGCCTG	1680
Db	1621		CAGCTGGGCAAGTCAACTGTCTTCTTTCCCTCACTGCTTGCCTCTCTTAAACGCCTG	1680
Qy	1681		CAGTGTGCTAGAGGACAAAAGAAAGTGAAGTCAGACATCCGCTTCTGCCCAAGATGCT	1740
Db	1681		CAGTGTGCTAGAGGACAAAAGAAAGTGAAGTCAGACATCCGCTTCTGCCCAAGATGCT	1740
Qy	1741		CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCAGTTGGTCAGCAGGCC	1800
Db	1741		CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCAGTTGGTCAGCAGGCC	1800
Qy	1801		TCTGTGTTTGGCACTGGCCCTGATTTGAATCTCGTCCACATTTGGAGAGCTCGGGGTGT	1860
Db	1801		TCTGTGTTTGGCACTGGCCCTGATTTGAATCTCGTCCACATTTGGAGAGCTCGGGGTGT	1860
Qy	1861		CCCTGGTTTTCCCTCTCGGAAATGAGCGCAGAGCCCTCGCTCTGAAAGACCGAGTG	1920
Db	1861		CCCTGGTTTTCCCTCTCGGAAATGAGCGCAGAGCCCTCGCTCTGAAAGACCGAGTG	1920
Qy	1921		TGGATGCCACTGGGCTAGTGTCTGGCCTCAGCTTCTTGCRAAGCTGTACAAAGAA	1980
Db	1921		TGGATGCCACTGGGCTAGTGTCTGGCCTCAGCTTCTTGCRAAGCTGTACAAAGAA	1980
Qy	1981		AAGACGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCTG	2040
Db	1981		AAGACGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCTG	2040
Qy	2041		CAGCTTTGACATCTTGGTGTAATCATGTGCTTCTCTTGTGTATACCCCTCCAGTATT	2100
Db	2041		CAGCTTTGACATCTTGGTGTAATCATGTGCTTCTCTTGTGTATACCCCTCCAGTATT	2100
Qy	2101		ACCAATTTGCCCTCACTGCCCTTGGTGAGCCCTTTAGTGCAAGACAGATGGGCTGTTT	2160
Db	2101		ACCAATTTGCCCTCACTGCCCTTGGTGAGCCCTTTAGTGCAAGACAGATGGGCTGTTT	2160
Qy	2161		TCCCCCACTCTGAGTAGTTGAGGTACATACAGAGCTCTTTTTTATTTGCCCTTTTCT	2220
Db	2161		TCCCCCACTCTGAGTAGTTGAGGTACATACAGAGCTCTTTTTTATTTGCCCTTTTCT	2220
Qy	2221		GCCTCTGAATGTTTCACTCTCGTCTCTTGTGTGAGGCGAGGAAGGGTGCCTCAGGG	2280
Db	2221		GCCTCTGAATGTTTCACTCTCGTCTCTTGTGTGAGGCGAGGAAGGGTGCCTCAGGG	2280
Qy	2281		GCCGCACTAGTATGATGCGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCACC	2340

Db	2281	GCCGACACTAGTATGATGCGAGTGTCCAGTGTGAACGACGAAATTAACATGTTGCAACC	2340
QY	2341	AAAAAAAAAAAAAAAAAAAA 	2356
Db	2341	AAAAAAAAAAAAAAAAAAAA 	2356

RESULT 2

```

US-08-905-223-188
; Sequence 188, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelt, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: other
; LOCATION: 165..302
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 93
; OTHER INFORMATION: region 33..170
; OTHER INFORMATION: id T50032
; OTHER INFORMATION: est
; FEATURE:
; NAME/KEY: other
; LOCATION: 291..339
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 97
; OTHER INFORMATION: region 160..208
; OTHER INFORMATION: id T50032
; OTHER INFORMATION: est
; FEATURE:
; NAME/KEY: other
; LOCATION: 132..172
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 97
; OTHER INFORMATION: region 1..41
; OTHER INFORMATION: id T50032

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: OTHER INFORMATION: est
:
: FEATURE:
:
: NAME/KEY: sig_peptide
: LOCATION: 71_139
: IDENTIFICATION METHOD: Von Heijne matrix
: OTHER INFORMATION: score4
: OTHER INFORMATION: seq QPILGTTTSVVTA/AL
US-08-905-223-188

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Query Match	13.1%;	Score 309;	DB 3;	Length 343;
Best Local Similarity	99.7%;	Pred. No. 4.5e-75;		
Matches 309;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

QY	1	ATCCTTGGGCGCACAGTCGGCCACCGGGGTCCGCCCGTCAATGGAGAGCGGAGCGCGC	60
Db	30	ATCCTTGGGCGCACAGTCGGCCACCGGGGTCCGCCCGTCAATGGAGAGCGGAGCGCGC	89
QY	61	CCTCGTGTGCCAGTTTCATCCTCCTGGGCACCACTCTGTGTACCGCGCCCTGTACT	120
Db	90	CCTCGTGTGCCAGTTTCATCCTCCTGGGCACCACTCTGTGTACCGCGCCCTGTACT	149
QY	121	CGGTGTACCGGAGAGGCCCGGGTCTCCCAAGAGCTCAAGGAGCTATAAAGTTCAAT	180
Db	150	CGGTGTACCGGAGAGGCCCGGGTCTCCCAAGAGCTCAAGGAGCTATAAAGTTCAAT	209
QY	181	TCGGTCAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATTCGCTTATGCTG	240
Db	210	TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATTCGCTTATGCTG	269
QY	241	TTATAGAAGGAGCTGTGCGGTCTGTTTAAAGAAACGCTTAAACGACAGTTTGTGGAAGACT	300
Db	270	TTATAGAAGGAGCTGTGCGGTCTGTTTAAAGAAACGCTTAAACGACAGTTTGTGGAAGACT	329
QY	301	GCAAGGGGGT	310
Db	330	GCAAGGGGGT	339

RESULT 3

US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 TWMTT


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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "cDNA of Pentin-1 optimized
; ORIGINAL SOURCE: for enhanced expression"
; ORGANISM: Pentaclethra macroloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1227
US-09-074-912-3

Query Match
Best Local Similarity 1.8%; Score 43.2; DB 3; Length 1227;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 703 TAAGCAGCCAGGACTTCGACGCTCTGACAGGCGAGGTCGAGCGTCAGGCTCTGGA 762
Db 158 TGATCTCTAAGCAGCTCGAGCGGACCTCCAGAGGTGGGACTCCAGCGCCAGGCTCGCG 217
QY 763 AGTGCTGGCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCCGGA 822
Db 218 AGTACTTCGACTGTGTGGCGGACCTCCACCGGGGCGCATCATCCGCCATCTCTCACCG 277
QY 823 AGCAGTATCTGACGCGGCGAGGCGCCTGCGC 854
Db 278 CCCCGGACCCGAGAACAGGACCCGCGCTC 309

```

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RESULT 6
US-09-290-136-3
; Sequence 3, Application US/09290136
; Patent No. 6339144
; GENERAL INFORMATION:
; APPLICANT: Cigan, Amy L.
; APPLICANT: Czapl, Thomas H.
; APPLICANT: Fallis, Lynn
; APPLICANT: Meyer, Terry E.
; APPLICANT: Mundell, Scott A.
; APPLICANT: Sabus, Brian
; APPLICANT: Schubert, Karel
; TITLE OF INVENTION: Proteins Having Insecticidal Activities and Methods of
; FILE REFERENCE: 5718-9A, 035718/180486
; CURRENT APPLICATION NUMBER: US/09/290.136
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: 09/074.912
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Pentaclethra macroloba
; FEATURE:
; OTHER INFORMATION: cDNA of Pentin-1 optimized for enhanced expression
; NAME/KEY: CDS
; LOCATION: (1)..(1227)
US-09-290-136-3

Query Match
Best Local Similarity 1.8%; Score 43.2; DB 3; Length 1227;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 703 TAAGCAGCCAGGACTTCGACGCTCTGACAGGCGAGGTCGAGCGTCAGGCTCTGGA 762
Db 158 TGATCTCTAAGCAGCTCGAGCGGACCTCCAGAGGTGGGACTCCAGCGCCAGGCTCGCG 217
QY 763 AGTGCTGGCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCCGGA 822
Db 218 AGTACTTCGACTGTGTGGCGGACCTCCACCGGGGCGCATCATCCGCCATCTCTCACCG 277

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QY 823 AGCAGTATCTGACGCGGCGAGGACGCGCTGCGC 854
Db 278 CCCCGGACCCGAGAACAGGACCCGCGCTC 309

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RESULT 7
US-09-270-767-10494
; Sequence 10494, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10494
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10494

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Query Match
Best Local Similarity 1.7%; Score 41.2; DB 4; Length 747;
Matches 121; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 710 CCAGGACTTCGACAGCCTGCTGCAGAGCGAGGTCGAGCGTCAGGCTCTGGAAGTGCT 769
Db 364 CCACGAGGACGAGGTCAGGTGATGAGGACGCTGTGCCCGGAGGCGGTGCT 423
QY 770 GCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCCGGAAGCAGTA 829
Db 424 GGATGAGAAATGGTGTCTAAGAGCGTGCACAGTGAAGGCGGAGGAGGAGGAGCGGT 483
QY 830 TCTGAGCGGCGAGGCGCTGCGCTTAACAGATGACGAGGAGGTTCCAGGAGCATGA 889
Db 484 TCAGCGGAGCAGGAGTGCACGATCGCAACAGCGCAAGTGAAGGAGGCGAAGGAGGA 543
QY 890 GCGCCAGCTGCTGAGCGGCGCAGCCTGAGGACGAGGAGTCTGAAGAGCGCTGTGT 949
Db 544 GCGGAGCGTTAAGCAGCAAGAACCTTGAGGCGAGGCGGCGGCGGATGC 603
QY 950 AGTGCTGTGAGCA 963
Db 604 CGAGCGCTGGCCA 617

```

```

RESULT 8
US-08-728-323A-1
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,323A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3489 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3489
 US-08-728-323A-1

Query Match 1.7%; Score 41; DB 2; Length 3489;
 Best Local Similarity 60.2%; Pred. No. 0.69;
 Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
 Db 1573 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632
 QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCCTGAGGACAGGAGAG 931
 Db 1633 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

RESULT 9

US-09-298-568-1
 Sequence 1, Application US/09298568
 Patent No. 6322792
 GENERAL INFORMATION:
 APPLICANT: Kieff, Elliott D.
 APPLICANT: Ballestas, Mary E.
 APPLICANT: Kaye, Kenneth M.
 TITLE OF INVENTION: RHADINO VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
 FILE REFERENCE: 16412-10001R
 CURRENT APPLICATION NUMBER: US/09/298,568
 CURRENT FILING DATE: 1999-04-21
 EARLIER APPLICATION NUMBER: US 60/109,422
 EARLIER FILING DATE: 1998-11-19
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3489
 TYPE: DNA
 ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-298-568-1

Query Match 1.7%; Score 41; DB 3; Length 3489;
 Best Local Similarity 60.2%; Pred. No. 0.69;
 Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
 Db 1573 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632
 QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCCTGAGGACAGGAGAG 931
 Db 1633 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

RESULT 10

US-09-410-399-1
 Sequence 1, Application US/09410399
 Patent No. 6482587
 GENERAL INFORMATION:
 APPLICANT: Robertson, Erle S.
 APPLICANT: Cotter, Murray A.
 TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
 FILE REFERENCE: UM-03778
 CURRENT APPLICATION NUMBER: US/09/410,399
 CURRENT FILING DATE: 1999-10-01
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3489
 TYPE: DNA
 ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-410-399-1

Query Match 1.7%; Score 41; DB 4; Length 3489;
 Best Local Similarity 60.2%; Pred. No. 0.69;
 Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
 Db 1573 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632
 QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCCTGAGGACAGGAGAG 931
 Db 1633 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

RESULT 11

US-09-894-273-1
 Sequence 1, Application US/09894273
 Patent No. 6756203
 GENERAL INFORMATION:
 APPLICANT: Kieff, Elliott D.
 APPLICANT: Ballestas, Mary E.
 APPLICANT: Kaye, Kenneth M.
 TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
 FILE REFERENCE: 16412-10001R
 CURRENT APPLICATION NUMBER: US/09/894,273
 CURRENT FILING DATE: 2001-06-28
 PRIOR APPLICATION NUMBER: US 60/109,422
 PRIOR FILING DATE: 1998-11-19
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3489
 TYPE: DNA
 ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-894-273-1

Query Match 1.7%; Score 41; DB 4; Length 3489;
 Best Local Similarity 60.2%; Pred. No. 0.69;
 Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
 Db 1573 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632
 QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCCTGAGGACAGGAGAG 931
 Db 1633 CAGCAGCAGGAGGCCACAGCAGGAGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

RESULT 12

US-08-770-379-20/c
 Sequence 20, Application US/08770379
 Patent No. 5849564


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; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
; TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 52342
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-20

Query Match 1.7%; Score 41; DB 2; Length 32207;
Best Local Similarity 60.2%; Pred. No. 2.2;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGCAGGCGCTGCTGAGCCGCAAGCCTGAGGACAGGGAGAG 931
Db 20424 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGGAGCCACAGCAGGAGCCCA 20365

QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCGCGGAGCCACAGCAGCGGGAGCCCGGAGCG 20312
Db 20364 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGCGGGAGCCCGGAGCG 20312

RESULT 13
US-08-757-669A-20/c
; Sequence 20, Application US/08/757669A
; Patent No. 6183751
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,669A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-669A-20

Query Match 1.7%; Score 41; DB 3; Length 32207;
Best Local Similarity 60.2%; Pred. No. 2.2;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGCAGGCGCTGCTGAGCCGCAAGCCTGAGGACAGGGAGAG 931
Db 20424 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGGAGCCCA 20365

QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCGCGGAGCCACAGCAGCGGGAGCCCGGAGCG 20312
Db 20364 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGCGGGAGCCCGGAGCG 20312

RESULT 14
US-09-230-371A-20/c
; Sequence 20, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 32207
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-230-371A-20

Query Match 1.7%; Score 41; DB 3; Length 32207;
Best Local Similarity 60.2%; Pred. No. 2.2;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGCAGGCGCTGCTGAGCCGCAAGCCTGAGGACAGGGAGAG 931
Db 20424 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGGAGCCCA 20365

QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCGCGGAGCCACAGCAGCGGGAGCCCGGAGCG 931
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Fri Nov 12 12:23:28 2004

Search completed: November 8, 2004, 02:54:14
Job time : 220 secs

Db 20364 CAGCAGCAGGAGCCACAGCAGCGGAGCCACAGCAGCGGAGCCCGCAGCAGCG 20312

RESULT 15
US-08-366-276-1
; Sequence 1, Application US/08366276
; Patent No. 5534409
; GENERAL INFORMATION:
; APPLICANT: Groner, Bernd
; APPLICANT: Gouilleux, Fabrice
; APPLICANT: Wakao, Hiroshi
; TITLE OF INVENTION: Cytokine Regulated Transcription Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,276
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409396.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scoot
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-19992/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2625
; OTHER INFORMATION: /product= "mammary gland factor"

Query Match 1.7%; Score 40.8; DB 1; Length 2818;
Best Local Similarity 50.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 102; CGGAGGAGGATGCT 607
QY 548 CATCGGCCACTACATCAGCGGTGAGCGGCCAAAGGCATCCAAAGAGACCGAGGAGATGCT 607
Db 1125 CAGAGCGGAGCACCTCTGCGCAGCAGCTGCCCATCCCGGCCCGCTGGAGGAGATGCTGC 1184
QY 608 GAAGGTGGGGGCCACCCCTCACAGGGGTTGGCGAACTGGTCTCTGGACAACTCTGTCCG 667
Db 1185 TGAGGTCAAGCCACCACATCAGGACATCATCTAGCCCTGGTGACCAGCACATTCATCAT 1244
QY 668 CTTGACGCCGCCCAACAAAGCATGCTACTATCTAAGCAGCCAGGACTTCGACAGCCT 727
Db 1245 CGAGAGCAGCCCGCTCAGGTCTTGAAGACCCAGACCAAGTTCCGGGCCACCGTGGCGCT 1304
QY 728 GCTGCAGAGCGAGGAGTCGAGCGT 751
Db 1305 GCTGTGGCGGGAAGCTGAACGT 1328

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OM protein - protein search, using sw model

Run on: November 6, 2004, 17:32:53 ; Search time 196 Seconds
(without alignments)
1033.326 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MSGGGRPSLCQFILLGTSV.....PKKCPICRQAITRIVILYNS 352

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	2	Q969V5
2	1824	99.6	352	2	Q72431
3	1818	99.3	352	2	Q9H9B5
4	1673	91.4	352	2	Q9VCW5
5	1672	91.3	352	2	Q8BHF2
6	1667	91.0	352	2	Q9DCV9
7	1277.5	69.8	353	2	Q6NTH6
8	1277.5	69.8	353	2	Aah68869
9	442.5	24.2	338	2	Q9VZJ9
10	436	23.8	339	2	Q7Q6A1
11	391.5	21.4	283	2	Q6PBA9
12	391.5	21.4	283	2	AAH59797
13	301	16.4	343	2	Q8L7N4
14	267.5	14.6	338	2	Q94HV7
15	266	14.5	341	2	Q9LQ59
16	230.5	12.6	237	2	Q9SLU0
17	201	11.0	383	2	Q9SVH3
18	166	9.1	376	2	Q99XR6
19	166	9.1	381	2	Q8CIP0
20	166	9.1	402	2	Q7QVP2
21	164.5	9.0	382	2	Q6GNI9
22	164	9.0	372	2	Q9H6W8
23	163	8.9	372	2	Q969K3
24	163	8.9	372	2	CAG33623
25	162.5	8.9	373	2	Q8NG47
26	162.5	8.9	372	2	Q80Z16
27	156	8.5	628	2	Q8UWD2
28	156	8.5	647	2	Q7TOK2
29	156	8.5	654	2	Q6ZM93
30	156	8.5	654	2	CAE47763
31	156	8.5	699	2	Q95TH2

32	155.5	8.5	303	2	Q96MX5
33	155.5	8.5	696	2	Q96MZ7
34	155.5	8.5	723	2	Q6UWE0
35	155.5	8.5	723	2	Q8NB40
36	155.5	8.5	723	2	Q96GT5
37	155.5	8.5	723	2	AAQ89189
38	151	8.2	319	2	Q8T0T5
39	151	8.2	700	2	Q9V6I3
40	147.5	8.1	330	2	Q6DDM0
41	144.5	7.9	327	2	Q8TBY7
42	144.5	7.9	618	1	BIR2_HUMAN
43	144.5	7.9	837	2	Q7PT21
44	143.5	7.8	310	2	Q96BE6
45	143.5	7.8	355	2	Q8NHWO

ALIGNMENTS

RESULT 1
Q969V5 PRELIMINARY; PRT; 352 AA.
AC Q969V5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein FLJ12875 (Hypothetical protein DKFZp762M0911).
DE DKFZp762M0911.
GN Name=FLJ12875; Synonyms=DKFZp762M0911;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fanev J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickinson M.C., Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC014010; AAH14010.1; -.

DR EMBL; BC010101; AAH10101.1; --
 DR EMBL; AL333989; CAD38745.1; --
 DR GO; GO:0004871; F:signal transducer activity; IMP.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IMP.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 352 AA; 39800 MW; 6EF2B8BFCB1801F CRC64;
 Query Match 100.0%; Score 1831; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-127; Indels 0; Gaps 0;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESGGRPSLCOFILLGTTTSVTAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 Db 1 MESGGRPSLCOFILLGTTTSVTAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 QY 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKQVWNRTHLWDCSKIIHQ 120
 Db 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKQVWNRTHLWDCSKIIHQ 120
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 ID Q72431
 AC Q72431
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative NFKB activating protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22646590; PubMed=12761501;
 RA Matsuda A., Suzuki Y., Honda G., Muramatsu S., Mutsuzaki O.,
 RA Nagano Y., Doi T., Shimotohno K., Harada T., Nishida E., Hayashi H.,
 RA Sugano S.;
 RT "Large-scale identification and characterization of human genes that
 activate NF-kappaB and MAPK signaling pathways.";
 RL Oncogene 22:3307-3318(2003).
 DR EMBL; AB097015; BAC77368.1;
 DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 SQ SEQUENCE 352 AA; 39784 MW; 6EF2B8ABBCBCE1801F CRC64;
 Query Match 99.6%; Score 1824; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 8.5e-127;

Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESGGRPSLCOFILLGTTTSVTAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 Db 1 MESGGRPSLCOFILLGTTTSVTAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 QY 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKQVWNRTHLWDCSKIIHQ 120
 Db 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKQVWNRTHLWDCSKIIHQ 120
 QY 121 TNPVFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 Db 121 TNPVFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 QY 181 GIOETEEMKVGATLTGVGELVDNNSVRLQPPQKQMYLLSQDPSLLQSQESSVRLW 240
 Db 181 GIOETEEMKVGATLTGVGELVDNNSVRLQPPQKQMYLLSQDPSLLQSQESSVRLW 240
 QY 241 KVLALVFGFATCATLFFILRKQYLRQERLRKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 Db 241 KVLALVFGFATCATLFFILRKQYLRQERLRKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 Db 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 RESULT 3
 Q9H9B5 PRELIMINARY; PRT; 352 AA.
 ID Q9H9B5
 AC Q9H9B5
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ12875.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14702039;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Karehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Terashima N., Sano S.,
 RA Moriya S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Ozaki Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Takahashi Y., Nakagawa K.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).

DR EMBL; AK02937; BAB14317.1; -
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 SQ SEQUENCE 352 AA; 39717 MW; C19F150D278C2DA9 CRC64;
 Query Match 99.3%; Score 1818; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 2.4e-126;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDLKSILSEAPG 60
 Db 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLQEHKVMWNRTHLWDCSKIIHOR 120
 Db 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLQEHKVMWNRTHLWDCSKIIHOR 120
 QY 121 TINTVPDLVPHEDGDVAVRVLPKPLDSVDLGLTVEYKFPSPQSFTDVIHYISGERPK 180
 Db 121 TINTVPDLVPHEDGDVAVRVLPKPLDSVDLGLTVEYKFPSPQSFTDVIHYISGERPK 180
 QY 181 GIQTEEMLVKGATLTGVLGELVLDNNSVRLQPPQGMQYLLSQDFDLSLQROESSVRLW 240
 Db 181 GIQTEEMLVKGATLTGVLGELVLDNNSVRLQPPQGMQYLLSQDFDLSLQROESSVRLW 240
 QY 241 KVLALVFGFATCATLFFILRKQYLQRLKQWEEFQHEAQLSRAPKPEDRESLKS 300
 Db 241 KVLALVFGFATCATLFFILRKQYLQRLKQWEEFQHEAQLSRAPKPEDRESLKS 300
 QY 301 ACVCLSFKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLVNS 352
 Db 301 ACVCLSFKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLVNS 352
 RESULT 4
 Q8VCM5 Q8VCM5 PRELIMINARY; PRT; 352 AA.
 ID Q8VCM5 PRELIMINARY; PRT; 352 AA.
 AC Q8VCM5 PRELIMINARY; PRT; 352 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE RIKEN cDNA 0610009K11.
 GN Name=0610009K11Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner R.L., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019516; AAH19516.1; -
 DR HSSP; P38398; 1JW7.
 DR MGD; MGI:1915600; 0610009K11Rik.
 DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 SQ SEQUENCE 352 AA; 39821 MW; F3FE5D4771E0B140 CRC64;
 Query Match 91.4%; Score 1673; DB 2; Length 352;
 Best Local Similarity 90.1%; Pred. No. 1.3e-115;
 Matches 317; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDLKSILSEAPG 60
 Db 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLQEHKVMWNRTHLWDCSKIIHOR 120
 Db 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLQEHKVMWNRTHLWDCSKIIHOR 120
 QY 121 TINTVPDLVPHEDGDVAVRVLPKPLDSVDLGLTVEYKFPSPQSFTDVIHYISGERPK 180
 Db 121 TINTVPDLVPHEDGDVAVRVLPKPLDSVDLGLTVEYKFPSPQSFTDVIHYISGERPK 180
 QY 181 GIQTEEMLVKGATLTGVLGELVLDNNSVRLQPPQGMQYLLSQDFDLSLQROESSVRLW 240
 Db 181 GIQTEEMLVKGATLTGVLGELVLDNNSVRLQPPQGMQYLLSQDFDLSLQROESSVRLW 240
 QY 241 KVLALVFGFATCATLFFILRKQYLQRLKQWEEFQHEAQLSRAPKPEDRESLKS 300
 Db 241 KVLALVFGFATCATLFFILRKQYLQRLKQWEEFQHEAQLSRAPKPEDRESLKS 300
 QY 301 ACVCLSFKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLVNS 352
 Db 301 ACVCLSFKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLVNS 352
 RESULT 5
 Q8BHF2 Q8BHF2 PRELIMINARY; PRT; 352 AA.
 ID Q8BHF2 PRELIMINARY; PRT; 352 AA.
 AC Q8BHF2 PRELIMINARY; PRT; 352 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:A830089D08 product:hypothetical RING finger containing
 DE protein, full insert sequence (Mus musculus 0 day neonate head cDNA,
 DE RIKEN full-length enriched library, clone:4831423H02
 DE product:hypothetical RING finger containing protein, full insert
 DE sequence) (Mus musculus adult male liver tumor cDNA, RIKEN full-length
 DE enriched library, clone:C730031H18 product:hypothetical RING finger
 DE containing protein, full insert sequence).
 GN Name=0610009K11Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
Kanno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Kondo H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Kondo H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
EMBL; AK083295; BAC38848.1; -.
HSSP; P38398; 1JM7
MGD; MGI:1915600; 0610009K1Rik.
GO; GO:0000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR001841; Znf_ring.
SMART; SM00184; RING; 1.
PROSITE; PSS0089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 39835 MW; 252530F1BD917871 CRC64;
Query Match 91.3%; Score 1672; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 1.5e-115;
Matches 316; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MESGSRPSLCQFILLGTTTSVTAALYSVYRQKARVSQELKGAQKVLHGLDLSILSEAPG 60
Db 1 MESGSRPSLQGVILLGTTSSMTAVLSYTRQKACQVQELKGAQKVLHGLDLSILSEAPG 60
Qy 61 KCVYAVTEGAVRSVKETLSQFVENCCKGVIRLTLOEHKMWNRTHLWDCSKIIHQ 120
Db 61 KCVYAVTEGAVRSVKETLSQFVENCCKGVIRLTLOEHKMWNRTHLWDCSKIIHQ 120
Qy 121 TNTVPFDLVPHEGVDVAVRVKPLDSVDLGLTVEYKFKPSIQSFTDVI GHYISGERPK 180
Db 121 TNTVPFDLVPHEGVDVAVRVKPLDSVDLGLTVEYKFKPSIQSFTDVI GHYISGERPK 180
Qy 181 GIQTEEMLVKVGATLTGVELVLDNNSVRLPPQKQMOYLLSSQDFDLSLORQESSVRLW 240
Db 181 GIQTEEMLVKVGATLTGVELVLDNNSVRLPPQKQMOYLLSSQDFDLSLORQESSVRLW 240
Qy 241 KVLALVFGFATCATLFFILRKOYLORQERLQKQOEFEHQAQLLRKPEDESLKS 300
Db 241 KVLALVFGFATCATLFFILRKOYLORQERLQKQOEFEHQAQLLRKPEDESLKS 300
Qy 301 ACVCLSLFSCVFLCCHGVSCCTCYRALPEPKPCICRQAITRVIPLYS 352
Db 301 ACVCLSLFSCVFLCCHGVSCCTCYRALPEPKPCICRQAITRVIPLYS 352
RESULT 6
Q9DCV9 PRELIMINARY; PRT; 352 AA.
AC Q9DCV9; 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DE library, clone:0610009K11 product:hypothetical RING finger containing
DE protein, full insert sequence.
OS Name=0610009K11Rik;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA the FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada M.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (KISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoch M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numata R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AK002416; BAB22084.1; --
DR HSSP; P38398; LJM7.
DR MGP; MGI:1915600; 0610009Klrlk.
DR GO; GO:0001015; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPRO01841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 39883 MW; 29933D46BD9165C6 CRC64;

Query Match 91.0%; Score 1667; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.6e-115;
Matches 315; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MESGGRSLCQFILLGTTVVVTAALYSVFYRKARVSOLKGAKVKHGLGDLKSTLSAPG 60
Db |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MESGRPSLGQVILGTSSMVTAVLYSIYRQAQVAQLKGAKIHLGDLKGLTSAPG 60

QY 61 KCVPYAVIEGAVRSVKETLNSQFVENCKGVIGTQRLTLOEHKVMWNRTLHWDCSKIIHQ 120
Db |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:
61 KCVPYAVIEGAVRSVKETLNSQFVENCKGVIGTQRLSQEHKVMWNRTLHWDCSKIIHQ 120

QY 121 TNTVPFDLVPHEDGDVDVAVRLKPLDSVDLCLETVYEKFHPSTQSFTDVI GHVIGSRPK 180
Db |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:
121 TNTVPFDLVPHEDGDVDVAVRLKPLDSVDLCLETVYEKFHPSTQSFTDVI GHVIGSRPK 180

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; RT
pr. proc Natl Acad Sci U.S.A. 99:16899-16903(2002).

[3]
RN
PP
SEQUENCE FROM N.A.

RC
RA
RA
TISSUE=Kidney;
Klein S., Strausberg R.;
submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC068869; AAH68869.1; -.
KW Hypothetical protein.
SQ SEQUENCE 353 AA; 40358 MW; 102A3C761CDD7EFA CRC64;

Query Match 69.8%; Score 1277.5; DB 2; Length 353;
Best Local Similarity 64.9%; Pred. No. 2.6e-89;
Matches 229; Conservative 63; Mismatches 60; Indels 1; Gaps

Qy
1 MESGGRPSLCQFILLGTTTSVVTAALYSVYRQKARVSQELGAKKKVHLGEDLSILSEAPG
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 MWCCGDSVCGLIITTSATLAVSVTVHKYRSVOTLLKAQKFCTDDLPALVSLDLPG

T MIENGGKFKFSVGVJHLLIOALIAHS *
61 KCVPYAVIEGAVRSVKETINSQFVNCKGVIQRLTIQEHKMVNRTTHLWDCSKI I HOR
QY

Db 61 KCPYAVIEGAVTSYKVELNSQYVENCKGVIQRLSLKEHKMVMNRTTHLWNDHEKIIHQK

Qy 121 TNTVPFDLVPHEDGVD-VAVRVLKPLDSDVLGLETVYVEKFHPSIQSFDTDVIGHVISGERP

Db 121 SNIVPFDLAPENPGESGVSVRVLRPLEAVDLGLETTIEYKFPAAVQSFNLSILGHYMTGERP
:
Qy 180 KGIQETEEMLKVGATLTGVCGLVLDNNSVRLQPPKQGMQYVLLSSQDFDSILLQROESSVRL

Db 181 KGVQTEEMLKIGARITGVGELVDNKTIKLQPPKQGLFYLLSSMDYEGCLLEKXQEVQMRW

QY 240 WRULALVFGFATCALFFILKRIQJGZARLWQZS
 : : : : : | : : : : :
DB 241 WRILSVFGVASCITFLFILRKRYHYKEQOHLKNLOREFEESRARQRVQQEPQNKEEVQ

QY 300 SACVVCCLSSFKSCVFLECGHVCSTCYRALPEPKKPCICQAITRVIPLYNS 352
 : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 301 NPCSLCTSKSCVFLECGHVCSTCSCYAALPSPKKPCICRNFDIVIPLYNS 353

RESULT 9
Q9VZJ9

ID	Q9VZJ9	PRELIMINARY;	PRT;	338 AA.
AC	Q9VZJ9;			
DT	01-MAY-2000	(TREMBlrel. 13, Created)		
ST	01 MAY 2000	(TREMBlrel. 13, Last sequence update)		

DI 01-MAY-2000 (trEMBLref. 27, last sequence update)
DT 05-JUL-2004 (trEMBLref. 27, last annotation update)
DE CG1134-PA (AT15655p).
GN ORFNames=CG1134;

OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Eubrachycera; Drosophilidae; *Drosophila*.

OC *epiphyas*Ordeu, *Protophormica*, *Protophormica*
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Coccaro P.A., Lewis S.F., Richards S., Ashburner M., Henderson S.N.,

RA George K.N., Lewis G.D., Macdonald S.P.,
RA Suttton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA

RA Abril J.F., Agpayani A., An H.J., Andrews-Pfannkuch C., Barlowin D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., German B.P., Bhandari D., Bolshakov S.,
RA Borikava D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
PA

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA

RA Dodson K., Doup L.E., Downes M., Dugan-Kocna S., Dumkov S.C., Dunn
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.

Query Match 69.8%; Score 1277.5; DB 2; Length 353;

Best Local Similarity 64.9%; Pred. No. 2.6e-86;
Matches 229; Conservative 63; Mismatches 60; Indels 1; Gaps 1;

1 MESGRPSICQFILLGTTTSVVTAALYSVYRQKARVSQELKGAKKVHLEDIKSILSEAPG 60

1	MENGRPSVGQVILLTSSAITALFYSIRHRYRSVQTLKARKFCLTDDLP	60
61	KCVPAVIEGAVRSVKETLNSQFVENCCKGVIORLTLQEHKMWNRTHLW	120
	NDCKSIHQ	

61	KCVFPAVIEGAVTSVKEVLASQYVENCIGVIRLSLKEHKVMVNRTHLLWMDHEKIIHQ	120
121	TNTVPFDIAPHEDGVD-VAVRVAKPLDSVDLGLETVYKEFHPSIQFTDVIQHYTSGRRP	179

```
db      : 121 SNTVPDLAPENPGESGVSVRVLRPLEAVDGLLETIYKFHPAQSFSNIIHLHYMTGERP 180
qy     : 180 KGIQETEEMLKVCATLTGVGELVDNNNSVRLRPPKQGMYLLSQDDFDSILQRQESSVRL 239
```

181 KGVQTEEMLKIGATITGVGELVLDNKTIKLPKDGMLFYLSSMDYEGLEKOEVMRW 240

QY WKV LAL VFG FAF CALLEF ILKRAQLDQA QENRANQQJST YAMHNGZSGLA
240 | : :: ||| : ||||| : || : || : ||| : | : : : ||| : :

Db 241 WRILSVFGVASCTTLFILRRKYRYHKQHKLNLQRFEESRARQRVQOEPONKEEVQ 300

Qy	300 SACVCLSSFKSVFLECHGVCSTECYRALPEPKKPCICRQAIRVIPLYNS 352 : : : : : : :
Db	301 NPFCISLCSTEKSVFLECHGVCSCISCYQALPSKKPCICRNFDRIVPILYS 353

RESULT 8
AAH68869

ID	AAH68869	PRELIMINARY;	PRT;	353 AA.
AC	AAH68869;			
DT	14-APR-2004	(TREMELrel.	27, Created)	

DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS *Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.

OX	NCBI TaxID=8333;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;

RA MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA Genomic and genomic tools for Yersinia research: The NIH Yersinia
RA Yersinia Research Center

Genetic and genomic tools for xenopus research and the xenopus initiative." ;
RT Dev. Dyn. 225:384-391 (2002) .
RN [2]

RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RX	MEDLINE=2238257; PubMed=12477932;
DA	Strausberg B, Feingold F A, Grouse L H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baba S., Tomiellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fancy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Kourguéz A.C., Grinnell
RA Krzywinski M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houson K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RL melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RL a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RL systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RL [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;

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Query Match 23.8%; Score 436; DB 2; Length 339;
 Best Local Similarity 31.5%; Pred. No. 5.1e-24;
 Matches 107; Conservative 67; Mismatches 148; Indels 18; Gaps 6;

QY 9 LCOFILLGTTSVVTAALYSYVRQKARVQSELGAKKVKHLGDLKLSILSEAPGKCVPAVIEGAV 68
 Db 4 LQEAVALIGDILLVWCSNQYKLRKNCRAKDAPQLQIDQDLADRLEKPEQDKLYAVI 63

QY 69 EGAVRSVKETLNQFVENCCKGVIOQLTQEHKVMVNRTHLWDCSKIIHQRVNTVPFDL 128
 Db 64 RGSVTPGTALRSAMSPSVGLQMTLTHLR-VARAMFGFWQEEKIHHVSANETFFRL 122

QY 129 VPHEGVDVAVRVLPKPLDSVDLGLTVEYKFPSPQSTFDTVIGHYISGERPKGIOETEM 188
 Db 123 VNGKQGV-IVSGLSABLDDMTVYENYEPSSLVFDHLFLGFSGRQKGLQTEEM 178

QY 189 LKVGATLTVGVELVLDNNSVRLQPPKQGMQYILSSQDFSLQORQESSVRLKWLALVFG 248
 Db 179 LRDSGFITAVGELEDDTGVRLHPPSNGWPMFLTATKSTLLKRLLEAKSSTLLKVLISG 238

QY 249 FATCATLFFILRKQYLQ-OBRLRLKQWQEFQHEAQLLSRAKPEDRESLKSAQV 303
 Db 239 TISAVLIVLITRKLYKRRKQWEEKLR-KQESRATRRARMRTTGLAEQ-LLCV 292

QY 304 VCLSFKSCVFLGCHVCSCTCYRALPEPKKPCICROAI 343
 Db 293 VCIYNPKVEICLPGHVCVLCENCAQKI--SLHCPVCRTVI 330

RESULT 11
 Q6PBA9 PRELIMINARY; PRT; 283 AA.

ID Q6PBA9
 AC Q6PBA9
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE LOC402879 protein (Fragment).
 GN Name=LOC402879;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting J., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC059797; AAH59797.1; -.
 FT NON_TER 1

FT SQ SEQUENCE 283 AA; 31798 MW; CD3C66BB7B68350C CRC64;
 Query Match 21.4%; Score 391.5; DB 2; Length 283;
 Best Local Similarity 37.2%; Pred. No. 8.1e-21;
 Matches 92; Conservative 45; Mismatches 103; Indels 7; Gaps 5;

QY 13 ILTGTTSVVTAALYSYVRQKARVQSELGAKKVKHLGDLKLSILSEAPGKCVPAVIEGAV 72
 Db 25 ICAGSCFARSGLFYKLYSDKLEVQKLIKEIPNPQDPDHLRLILNASSNKLHYVAVEGLV 84

QY 73 RSVKETLNSQFVENCCKGVIOQLTQEHKVMVNRTHLWDCSKIIH--QRTNTPPDLV- 129
 Db 85 QAVGEPISSQVPRCHGVIOKITVHEHWKYWNSLLKSW--VSKVKNQQTNTNTPVFLVQ 142

QY 130 PHEDGVAVRVLPKPLDSVDLGLTVEYKFPSPQSTFDTVIGHYISGERPKGIOETEM 189
 Db 143 PGSFISVQVVRVSPLEASGDFLQVHRRVNRNAKEGLMDVGLGISEKPIALSEREDLL 202

QY 190 KVGATLTVGVELVLDNNSVRLQPPKQGMQYILSSQDFSLQORQESSVRLKWLALVFG 248
 Db 203 RVGVPPLTAFGLVLEQEKIMRIQPKDGRSFLVPSDYNSPMORHONSVMNMKGLTVLFG 262

QY 249 FATCATL 255
 Db 263 L-TGSTL 268

RESULT 12
 AAH59797 PRELIMINARY; PRT; 283 AA.

ID AAH59797
 AC AAH59797
 DT 03-MAR-2004 (Tremblrel. 27, Created)
 DT 03-MAR-2004 (Tremblrel. 27, Last sequence update)
 DT 03-MAR-2004 (Tremblrel. 27, Last annotation update)
 DE LOC402879 protein (Fragment).
 GN LOC402879;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting J., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC059797; AAH59797.1; -.
 FT NON_TER 1

[illegible]

Fri Nov 12 12:23:32 2004

Best Local Similarity 27.3%; Pred. No. 2e-11;
Matches 97; Conservative 64; Mismatches 136; Indels 58; Gaps 19;
QY 24 ALYSVVRQKARVSOELGAKVHLGDLKILSEAPGKCVPYAVIEGAVRSVKETLNSQF 83
Db 15 ALYLLTRSTGR---DIKSTRVYQKLEQLV-EVESKVVPLII-----AVSGDVGSET 64
QY 84 VENCK-----GVIOQLTLQEHKVMWNRTHLWDCSKIIHQTNTVPFDLVPHEDGDVDA 138
Db 65 PIKCEHSYVLGVFLKRT-AEQVLRNRWFSWVRNSTLMQPMTEKVPWYL---DDGTG-- 118
QY 139 VRVLKPLDSVDLGL-----ETVYEKHPISQSFDTDVIGHYISGERPKGIQETEMLKVGA 193
Db 119 -RVNVDVSQGLGLALTGVSDVFEKAP-VSLVQVQALG-YLKGFILGVHRHVERVPIGT 175
QY 194 TLTVGELVLDN-NSVRLQPPKQGMQVYLLSQDSDLQROESSVRLWKVLAAL---VFGF 249
Db 176 PLTVVGEAVRDMGNVRIOKPEQG-PFYVTIPLDLQILSKGLDLSRRFKYASMGITVLGV 234
QY 250 ATCA--TLFFTLRK--QVLOQRER-LRLKQMOEEFQEHQAQLLSRAKPEDRES----- 297
Db 235 ILISKPVIEYILKRIEDTLERRRQFALKRVVD-----AAARRAKPVTGGSGTSRD 287
QY 298 --LKSACVVLSSFKSCVFLGCHVSCTECYRALPEPKKCPICQAITRVIPLY 350
Db 288 GDTPLCVCLDQKYNATAFVCGHMCCTPCSLQL---RTCPLCRERIQQVLKIY 339

Search completed: November 6, 2004, 17:42:25
Job time : 200 secs

SQ SEQUENCE 338 AA; 37729 MW; BA5598FB4C0D296C CRC64;
Query Match 14.6%; Score 267.5; DB 2; Length 338;
Best Local Similarity 27.5%; Pred. No. 1.5e-11;
Matches 97; Conservative 66; Mismatches 133; Indels 57; Gaps 20;
QY 24 ALYSVVRQKARVSOELGAKVHLGDLKILSEAPGKCVPYAVIEGAVRSVKETLNSQF 83
Db 15 ALYLLTRSTGR---DIKSTRVYQKLEQLV-EVESKVVPLII-----AVSGDVGSET 64
QY 84 VENCK-----GVIOQLTLQEHKVMWNRTHLWDCSKIIHQTNTVPFDLVPHEDGDVDA 138
Db 65 PIKCEHSYVLGVFLKRT-AEQVLRNRWFSWVRNSTLMQPMTEKVPWYL---DDGTG-- 118
QY 139 VRVLKPLDSVDLGL-----ETVYEKHPISQSFDTDVIGHYISGERPKGIQETEMLKVGA 193
Db 119 -RVNVDVSQGLGLALTGVSDVFEKAP-VSLVQVQALG-YLKGFILGVHRHVERVPIGT 175
QY 194 TLTVGELVLDN-NSVRLQPPKQGMQVYLLSQDSDLQROESSVRLWKVLAAL---VFGF 249
Db 176 PLTVVGEAVRDMGNVRIOKPEQG-PFYVTIPLDLQILSKGLDLSRRFKYASMGITVLGV 234
QY 250 ATCA--TLFFTLRK--QVLOQRER-LRLKQMOEEFQEHQAQLLSRAKPEDRES----- 297
Db 235 ILISKPVIEYILKRIEDTLERRRQFALKRVVD-----AAARRAKPVTGGSGTSRD 287
QY 298 LKSACVVLSSFKSCVFLGCHVSCTECYRALPEPKKCPICQAITRVIPLY 350
Db 288 -PDLVCVCLDQKYNATAFVCGHMCCTPCSLQL---RTCPLCRERIQQVLKIY 336

RESULT 15

Q9LQ59 PRELIMINARY; PRT; 341 AA.
AC Q9LQ59;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE T30816.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
RA Altati H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Lueros S.,
RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
RA Federspiel N.A., Theologis A., Ecker J.R.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Chao Q., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC009317; AAF79749.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 341 AA; 38017 MW; 6511F8370A7B5450 CRC64;

Query Match 14.5%; Score 266; DB 2; Length 341;

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: November 8, 2004, 01:00:43 ; Search time 3839 Seconds
 (without alignments)
 3304.240 Million cell updates/sec
 Title: US-09-978-360A-32
 Perfect score: 2356
 Sequence: 1 atccctggccacagtcgg.....aaccaaaaaaaaaaaaaa 2356
 Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 3611042 seqs, 2692057975 residues
 Total number of hits satisfying chosen parameters: 7222084
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	100.0	2356	11	US-09-978-360A-32
2	2356	100.0	2356	15	US-10-315-664-55
3	2338.4	99.3	2413	16	US-10-169-395-112
4	2336.8	99.2	2401	15	US-10-024-298A-76
5	2336.8	99.2	2401	15	US-10-042-211A-76
6	2336.8	99.2	2401	16	US-10-617-217A-76
7	2336.8	99.2	2401	18	US-10-024-298A-76
8	2335.2	99.1	2401	15	US-10-024-298A-74
9	2335.2	99.1	2401	15	US-10-042-211A-74
10	2335.2	99.1	2401	16	US-10-617-217A-74
11	2335.2	99.1	2401	18	US-10-024-298A-74
12	2330.8	98.9	2446	9	US-09-764-864-14

13	2217	94.1	2377	16	US-10-221-625-132	Sequence 132, App
14	1766	75.0	1791	9	US-09-764-864-475	Sequence 475, App
15	1751.4	74.3	1780	16	US-10-264-237-1275	Sequence 1275, App
16	1059	44.9	1059	16	US-10-169-395-102	Sequence 102, App
17	435	18.5	435	15	US-10-206-901B-36	Sequence 36, Appl
18	363	15.4	374	9	US-09-983-965-5476	Sequence 1321, Ap
19	290.8	12.3	398	9	US-09-983-965-5476	Sequence 5476, Ap
20	195.2	8.3	260	16	US-10-242-535A-4864	Sequence 4864, Ap
21	195.2	8.3	260	16	US-10-085-783A-4864	Sequence 4864, Ap
22	162.4	6.9	175	16	US-10-242-535A-2905	Sequence 2905, Ap
23	162.4	6.9	175	16	US-10-085-783A-2905	Sequence 2905, Ap
24	105.6	4.5	167	9	US-09-783-590-11630	Sequence 11630, A
25	60	2.5	60	10	US-09-908-975-13122	Sequence 13122, A
26	47.2	2.0	88232	13	US-10-087-192-1599	Sequence 1699, Ap
27	45.8	1.9	1239	15	US-10-214-446-35	Sequence 35, Appl
28	45.8	1.9	18438	15	US-10-156-761-2886	Sequence 2886, Ap
29	45.8	1.9	125746	15	US-10-156-761-15102	Sequence 15102, A
30	45.8	1.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
31	45.4	1.9	412	9	US-09-983-965-4755	Sequence 4755, Ap
32	44.4	1.9	2436	15	US-10-369-493-43090	Sequence 43090, A
33	43	1.8	2076	15	US-10-156-761-4305	Sequence 4305, App
34	43	1.8	3710	17	US-10-322-281-599	Sequence 599, App
35	43	1.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
36	42.8	1.8	1716	16	US-10-260-238-1227	Sequence 1227, Ap
37	42.8	1.8	1737	17	US-10-437-963-8794	Sequence 8794, Ap
38	42.4	1.8	2511	17	US-10-437-963-78199	Sequence 78199, A
39	42.2	1.8	2556	18	US-10-425-115-88564	Sequence 88564, A
40	42	1.8	594	14	US-10-123-155-10	Sequence 10, Appl
41	42	1.8	594	15	US-10-146-731-10	Sequence 10, Appl
42	42	1.8	594	15	US-10-140-472-10	Sequence 10, Appl
43	42	1.8	594	15	US-10-141-761-10	Sequence 10, Appl
44	42	1.8	594	15	US-10-142-885-10	Sequence 10, Appl
45	42	1.8	594	15	US-10-158-790-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-978-360A-32
 ; Sequence 32, Application US/09978360A
 ; Publication No. US20040110939A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
 ; APPLICANT: Duclert, Aymeric
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Jobert, Severin
 ; APPLICANT: Clusel, Catherine
 ; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
 ; FILE REFERENCE: 56.USA.CIP
 ; CURRENT APPLICATION NUMBER: US/09/978,360A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: US 60/066,677
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: US 60/069,957
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: US 60/074,121
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: US 60/081,563
 ; PRIOR FILING DATE: 1998-04-13
 ; PRIOR APPLICATION NUMBER: US 60/096,116
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: US 60/099,273
 ; PRIOR FILING DATE: -09-04
 ; PRIOR APPLICATION NUMBER: US 09/191,997
 ; PRIOR FILING DATE: 1998-11-13
 ; PRIOR APPLICATION NUMBER: US 09/215,435
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: PCT/IB98/02122
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: US 09/247,155
 ; PRIOR FILING DATE: 1999-02-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 810

SOFTWARE: Patent.pm

SEQ ID NO 32

LENGTH: 2356

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 42...1097

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 42...110

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 4.40

OTHER INFORMATION: seq QFILLGTTSSVVA/AL

FEATURE:

NAME/KEY: polyA_signal

LOCATION: 2323...2328

FEATURE:

NAME/KEY: polyA_site

LOCATION: 2341...2356

US-09-978-360A-32

Query Match 100.0%; Score 2356; DB 11; Length 2356;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATCCTTGGCGGCACAGTGGCCACCGGGCTCGCCGCGTCAATGAGAGCGGAGGCGGC	60
DB	1	ATCCTTGGCGGCACAGTGGCCACCGGGCTCGCCGCGTCAATGAGAGCGGAGGCGGC	60
QY	61	CCTCGCTGCGCAGTTCATCCCTCTGGGCAACACCTCTGTGTCAACCGCCCTGTACT	120
DB	61	CCTCGCTGCGCAGTTCATCCCTCTGGGCAACACCTCTGTGTCAACCGCCCTGTACT	120
QY	121	CGGTGTACCGGAGAAAGCGCGGTCTCCAGAGCTCAAGGAGCTAAAGATTCAAT	180
DB	121	CGGTGTACCGGAGAAAGCGCGGTCTCCAGAGCTCAAGGAGCTAAAGATTCAAT	180
QY	181	TGGGTGAAGATTAAAGATATCTTTTCAAGAGCTCCAGGAAATCGTGCCTTATGCTG	240
DB	181	TGGGTGAAGATTAAAGATATCTTTTCAAGAGCTCCAGGAAATCGTGCCTTATGCTG	240
QY	241	TTATAGAAGAGCTGTGCGGTCTGTAAAGAAACGCTTAACACCGAGTTGTGGAACCT	300
DB	241	TTATAGAAGAGCTGTGCGGTCTGTAAAGAAACGCTTAACACCGAGTTGTGGAACCT	300
QY	301	GCAAGGGGTAATTCAGCGGCTGACATTCAGGAGCAACAGATGTTGGAATCGAACCA	360
DB	301	GCAAGGGGTAATTCAGCGGCTGACATTCAGGAGCAACAGATGTTGGAATCGAACCA	360
QY	361	CCACCTTTGGAATGATGCTCAAGATCAATTCATCAGAGCAACACAGTGCCTTTG	420
DB	361	CCACCTTTGGAATGATGCTCAAGATCAATTCATCAGAGCAACACAGTGCCTTTG	420
QY	421	ACCTGTGTGCCACGAGAGTGGGTGATGCTGTGCGAGTCTGAAGCCCTGGAAT	480
DB	421	ACCTGTGTGCCACGAGAGTGGGTGATGCTGTGCGAGTCTGAAGCCCTGGAAT	480
QY	481	CAGTGTGCTGGGTCTAGAGCTGTGTATGAGAATTCACCCCTCGATTTCAGTCTCA	540
DB	481	CAGTGTGCTGGGTCTAGAGCTGTGTATGAGAATTCACCCCTCGATTTCAGTCTCA	540
QY	541	CCGATGTCATCGGCCTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600
DB	541	CCGATGTCATCGGCCTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600
QY	601	AGATGCTGAAGTGGGGGCCACCTCTCACAGGGGTGGCGAACTGGTCTGGACACAACT	660
DB	601	AGATGCTGAAGTGGGGGCCACCTCTCACAGGGGTGGCGAACTGGTCTGGACACAACT	660
QY	661	CTGTCCGCTGACGGCGCCCAACAGGATGCTACTATCTAAGAGCGGAGGACTTCG	720

DB	661	CTGTCCGCTGACGGCGCCCAACAAAGGATGCGTACTATCTAAGACGACGAGCTTCG	720
QY	721	ACAGCCTGTGACAGAGGAGGAGTTCGAGGCTCTGGAAGTGTGCGCCTGGTTT	780
DB	721	ACAGCCTGTGACAGAGGAGGAGTTCGAGGCTCTGGAAGTGTGCGCCTGGTTT	780
QY	781	TTGGCTTTGCCACATGTGCCACCTCTTCTTCAATCTCCGGAAGCATCTCCAGCGGC	840
DB	781	TTGGCTTTGCCACATGTGCCACCTCTTCTTCAATCTCCGGAAGCATCTCCAGCGGC	840
QY	841	AGGAGCGCTTGGCGCTCAAGCAGATGAGGAGGAGTTCAGGAGCATGAGGCCAGCTGC	900
DB	841	AGGAGCGCTTGGCGCTCAAGCAGATGAGGAGGAGTTCAGGAGCATGAGGCCAGCTGC	900
QY	901	TGAGCCGAGCAAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTGTCTGA	960
DB	901	TGAGCCGAGCAAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTGTCTGA	960
QY	961	GCAGCTTCAAGTCTCGCTCTTTCTGAGTGTGGGACGTTTCTTCTGACCCGAGTGT	1020
DB	961	GCAGCTTCAAGTCTCGCTCTTTCTGAGTGTGGGACGTTTCTTCTGACCCGAGTGT	1020
QY	1021	ACCGCGCTTGCAGAGCGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA	1080
DB	1021	ACCGCGCTTGCAGAGCGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA	1080
QY	1081	TACCCCTGTACAAACAGCTTAATAGTTTGAAGCGCACAGCTTGACCTGGAAGCACCCCTG	1140
DB	1081	TACCCCTGTGTACAAACAGCTTAATAGTTTGAAGCGCACAGCTTGACCTGGAAGCACCCCTG	1140
QY	1141	CCCCCTTTTCAGGGATTTTATCTCGAGGCTTTTGGAGGAGGAGTGGTGGGGTGTGT	1200
DB	1141	CCCCCTTTTCAGGGATTTTATCTCGAGGCTTTTGGAGGAGGAGTGGTGGGGTGTGT	1200
QY	1201	CACCTCCAGGATGATGAGGAGGAAATGGGTAGAACTCTCCAGACCCATGCTCCAA	1260
DB	1201	CACCTCCAGGATGATGAGGAGGAAATGGGTAGAACTCTCCAGACCCATGCTCCAA	1260
QY	1261	TGCGAGGATGCTGCCTTTCCACCTGAGAGGAGGAGGCTTCCATGTGACGCTCATCAG	1320
DB	1261	TGCGAGGATGCTGCCTTTCCACCTGAGAGGAGGAGGCTTCCATGTGACGCTCATCAG	1320
QY	1321	GCCTCACCTCGGAGGATGCGGTGCTCTCCAGGAGGAGGAGTGTGAGGAGTGTG	1380
DB	1321	GCCTCACCTCGGAGGATGCGGTGCTCTCCAGGAGGAGGAGTGTGAGGAGTGTG	1380
QY	1381	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGTGAGGAGTGTGAGGAGTGTG	1440
DB	1381	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGTGAGGAGTGTGAGGAGTGTG	1440
QY	1441	TGTCTTCTGTTTTTTTCTGGTGAATCGTTGCTGTGCTGTGCTGTGAGGAGTGTG	1500
DB	1441	TGTCTTCTGTTTTTTTCTGGTGAATCGTTGCTGTGCTGTGCTGTGAGGAGTGTG	1500
QY	1501	GGGAGGAAAGGCTGGGCGCCGAGTCAACCGATGCTGTGCTGTGCTGTGAGGAGTGTG	1560
DB	1501	GGGAGGAAAGGCTGGGCGCCGAGTCAACCGATGCTGTGCTGTGCTGTGAGGAGTGTG	1560
QY	1561	CTGCGGAGCTTTTCTTCTTTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
DB	1561	CTGCGGAGCTTTTCTTCTTTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
QY	1621	CAGGCTGGGAGGTCAACTTGTGTCTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1680
DB	1621	CAGGCTGGGAGGTCAACTTGTGTCTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1680
QY	1681	CACGTGTGTGAGGAGCAAAAGAGTGAAGTCAAGGAGGAGTGTGAGGAGGAGTGTG	1740
DB	1681	CACGTGTGTGAGGAGCAAAAGAGTGAAGTCAAGGAGGAGTGTGAGGAGGAGTGTG	1740
QY	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGGAGTGTGAGGAGGAGTGTG	1800
DB	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGGAGTGTGAGGAGGAGTGTG	1800

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QY 1801 TCTGGTTTCCCACTGCGCTGATTTGAATCTCTGCACTTGGAGAGCTCGGGTGGT 1860
Db 1801 TCTGGTTTCCCACTGCGCTGATTTGAATCTCTGCACTTGGAGAGCTCGGGTGGT 1860
QY 1861 CCTGGTTTCCCTCCCTGGAGATGAGGCGAGGCTCGCTCTCTGAAGACGCAAGT 1920
Db 1861 CCTGGTTTCCCTCCCTGGAGATGAGGCGAGGCTCGCTCTCTGAAGACGCAAGT 1920
QY 1921 TGGATGCCACTGCGCTAGTCTCTGGCTCAGAGCTTCCTTGAAGCTGTCAAGAA 1980
Db 1921 TGGATGCCACTGCGCTAGTCTCTGGCTCAGAGCTTCCTTGAAGCTGTCAAGAA 1980
QY 1981 AAGCAGCGGCTGGCACTGAGCATATGCGCTCTTGGGCTCCCTCATCCAGCCGCTG 2040
Db 1981 AAGCAGCGGCTGGCACTGAGCATATGCGCTCTTGGGCTCCCTCATCCAGCCGCTG 2040
QY 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCTCTCTTGTGTACCCCTCCAGTATT 2100
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Db 2101 ACCATTGGCCCTCACTGCGCTTGGTGTAGGCTTTTAGTGCAAGACAGATGGGGCTGTTT 2160
QY 2161 TCCGCCACTCTGAGTAGTGGAGTCAATACAGCTCTTTTATTGCCCCCTTTCT 2220
Db 2161 TCCGCCACTCTGAGTAGTGGAGTCAATACAGCTCTTTTATTGCCCCCTTTCT 2220
QY 2221 GCCTCTGATGTTTCACTCTCTGCTCTCTTGTGCGAGGAGGAGGCTCGCTCAGG 2280
Db 2221 GCCTCTGATGTTTCACTCTCTGCTCTCTTGTGCGAGGAGGAGGCTCGCTCAGG 2280
QY 2281 GCCGACACTAGTATGATGAGTGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2340
Db 2281 GCCGACACTAGTATGATGAGTGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2340
QY 2341 AAAAAAAAAAAAAA 2356
Db 2341 AAAAAAAAAAAAAA 2356
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; Sequence 55, Application US/10315664
; Publication No. US20030203377A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: GNSSET.050CP3
; CURRENT APPLICATION NUMBER: US/10/315,664
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/599,360
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 55
; LENGTH: 2356
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..1097
; FEATURE:
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; OTHER INFORMATION: score 4.40
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; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 2323..2328
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; NAME/KEY: polyA_site
; LOCATION: 2341..2356
US-10-315-664-55

Query Match 100.0%; Score 2356; DB 15; Length 2356;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCCGCTCATGGAGAGCGAGGCGGC 60
QY 61 CCTCGCTGTGCCAGTTCATCCTCTCTGGGCAACCACTCTGTGTGTCACCGCCCTGTACT 120
Db 61 CCTCGCTGTGCCAGTTCATCCTCTCTGGGCAACCACTCTGTGTGTCACCGCCCTGTACT 120
QY 121 CCGTGTACCGGCAGAAAGCGCCGCTCTCCCAAGAGCTCAAGGAGCTAAAAAGTTCATT 180
Db 121 CCGTGTACCGGCAGAAAGCGCCGCTCTCCCAAGAGCTCAAGGAGCTAAAAAGTTCATT 180
QY 181 TGGGTGAAGATTTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTGCTTATGCTG 240
Db 181 TGGGTGAAGATTTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTGCTTATGCTG 240
QY 241 TTATAGAGGAGCTGTGCGGCTGTGTTAAAGAAACGCTTAAACAGCAGTTTGTGAAAACT 300
Db 241 TTATAGAGGAGCTGTGCGGCTGTGTTAAAGAAACGCTTAAACAGCAGTTTGTGAAAACT 300
QY 301 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGGAGCACAAGATGTTGGATCGAACCA 360
Db 301 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGGAGCACAAGATGTTGGATCGAACCA 360
QY 361 CCCACCTTTGGAATGATTTGCTCAAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG 420
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QY 421 ACCTGTGCCCCACGAGATGCGCTGTGATGCGTGTGCGAGTCTGAAGCCCTGGAAT 480
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1861 CCCTGTTTTCCTTCTGGAATGAGGCGCAGAGGCTCGCTCTCTGAAGAGCAGTGT 1920
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1921 TGGATGCACTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

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RESULT 3
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; Sequence 112, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING
; TITLE OF INVENTION: THESE PROTEINS
; FILE REFERENCE: 01997.015100.US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/JP00/09359
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 150
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; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1173)
; US-10-169-395-112

Query Match 99.3%; Score 2338.4; DB 16; Length 2413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	194	CCGTGTACCGGCAAGAGCCCGGGTCTCCAAAGAGTCAAGGAGCTCAAAAAGTTCA TT	253
Qy	181	TGGGTGAAGATTTTAAAGAGTATCTTTTCAGAAAGCTCCAGAAATCGTGTCTTATGCTG	240
Db	254	TGGGTGAAGATTTTAAAGAGTATCTTTTCAGAAAGCTCCAGAAATCGTGTCTTATGCTG	313
Qy	241	TTATAGAAGAGCTGTGCGGCTCTGTAAAGAAACGCTTAACAGCAGTTTGTGGAACCT	300
Db	314	TTATAGAAGAGCTGTGCGGCTCTGTAAAGAAACGCTTAACAGCAGTTTGTGGAACCT	373
Qy	301	GCNAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAGATGGTGTGGAATCGAACCA	360
Db	374	GCNAGGGGGTAATTCAGCGGCTGACACTTCAGGAGCACAGATGGTGTGGAATCGAACCA	433
Qy	361	CCACACTTTGGAAATGATTCCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	420
Db	434	CCACACTTTGGAAATGATTCCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	493
Qy	421	ACTGTGTGCCCAACAGGATGCGTGGATGTGGCTGTGCGAGTGTGAGCGCCCTGGACT	480
Db	494	ACTGTGTGCCCAACAGGATGCGTGGATGTGGCTGTGCGAGTGTGAGCGCCCTGGACT	553
Qy	481	CAGTGGATCTGGTCTAGAGACTGTGTATGAAAGTTCCACCCCTCGATTCACTCTTCA	540
Db	554	CAGTGGATCTGGTCTAGAGACTGTGTATGAAAGTTCCACCCCTCGATTCACTCTTCA	613
Qy	541	CCGATGTCAATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGACCGAGG	600
Db	614	CCGATGTCAATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGACCGAGG	673
Qy	601	AGATCCTGAAGTGGGGGCCACCTTCACAGGGGTTGGCGAACTGGTCTCTGACACAACT	660
Db	674	AGATCCTGAAGTGGGGGCCACCTTCACAGGGGTTGGCGAACTGGTCTCTGACACAACT	733
Qy	661	CTGTCGGCTCTGAGCGCGCCCAACAGGATGAGTACTATCTAAGCAGCCAGGACTTCG	720
Db	734	CTGTCGGCTCTGAGCGCGCCCAACAGGATGAGTACTATCTAAGCAGCCAGGACTTCG	793
Qy	721	ACAGCCTCTGTCAGAGGCAGAGTCGAGCGTCAGGCTCTGGAAGTGTGCGCTGTTT	780
Db	794	ACAGCCTCTGTCAGAGGCAGAGTCGAGCGTCAGGCTCTGGAAGTGTGCGCTGTTT	853
Qy	781	TTGGTTTGGCAATGTGCCACCTCTTCTTTCATTTCCGGAAGCAGTATCTGCAGCGCG	840
Db	854	TTGGTTTGGCAATGTGCCACCTCTTCTTTCATTTCCGGAAGCAGTATCTGCAGCGCG	913
Qy	841	AGGAGCGCTCGGCTCTAAGCAGATGAGGAGGATTCAGGACATAGAGCCAGCTGC	900
Db	914	AGGAGCGCTCGGCTCTAAGCAGATGAGGAGGATTCAGGACATAGAGCCAGCTGC	973
Qy	901	TGAGCCGAGCCAAAGCCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTCTGTA	960
Db	974	TGAGCCGAGCCAAAGCCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTCTGTA	1033
Qy	961	GCAGCTTCAAGTCTCGGCTCTTTCTGAGATGTGGGCACGTTTGTTCCTGCACCGAGTCT	1020
Db	1034	GCAGCTTCAAGTCTCGGCTCTTTCTGAGATGTGGGCACGTTTGTTCCTGCACCGAGTCT	1093
Qy	1021	ACCGGCTTTGCCAGAGCCCAAGATGCCCCATCTCGACACAGGCGATCACCCGGTGA	1080
Db	1094	ACCGGCTTTGCCAGAGCCCAAGATGCCCCATCTCGACACAGGCGATCACCCGGTGA	1153
Qy	1081	TACCCCTGTACAAACAGCTTAATAGTTTGGAGCGGCACAGCTTGACTTGGAGCACCCCTG	1140
Db	1154	TACCCCTGTACAAACAGCTTAATAGTTTGGAGCGGCACAGCTTGACTTGGAGCACCCCTG	1213

QY	1141	CCCCCTTTTCAGGGATTTTATCTCGAGCCTTTTGGAGGAGCAGTGGTGGGGGTAGCTGT	1201
Db	1214	CCCCCTTTTCAGGGATTTTATCTCGAGCCTTTTGGAGGAGCAGTGGTGGGGGTAGCTGT	1273
QY	1201	CACCTCCAGGTATGATTCAGGGAGAAATTGGTAGAAACTTCCAGACCCATGCCCTCCAA	1260
Db	1274	CACCTCCAGGTATGATTCAGGGAGAAATTGGTAGAAACTTCCAGACCCATGCCCTCCAA	1333
QY	1261	TGGCAGGATGCTGCTCTTTCCCACTTGAGAGGGGACCTTGTCTCATGTGACGACCTCATCAGA	1320
Db	1334	TGGCAGGATGCTGCTCTTTCCCACTTGAGAGGGGACCTTGTCTCATGTGACGACCTCATCAGA	1393
QY	1321	GCCTCACCTCGGAGGATGCCGTGCGCTCTCTCCAGAGCCAGATCAGTGCAGTGTG	1380
Db	1394	GCCTCACCTCGGAGGATGCCGTGCGCTCTCTCCAGAGCCAGATCAGTGCAGTGTG	1453
QY	1381	ACTGAAATGCTCATCACATTAAAGCACAAAGCCAGTGATCAGAGCTTCTTGTTCCTG	1440
Db	1454	ACTGAAATGCTCATCACATTAAAGCACAAAGCCAGTGATCAGAGCTTCTTGTTCCTG	1511
QY	1441	TGCTCTCTGTTTTTTTCTGTGTAATCGTTGCTGTGCTGTGGACTTCGTGAGACACTCAGAG	1500
Db	1514	TGCTCTCTGTTTTTTTCTGTGTAATCGTTGCTGTGCTGTGGACTTCGTGAGACACTCAGAG	1573
QY	1501	GGAGGAAAGCTTGGGCCCCGAGTACAACGGATGCTTTGGGTGCTGCTCCGAAAGAGACT	1560
Db	1574	GGAGGAAAGCTTGGGCCCCGAGTACAACGGATGCTTTGGGTGCTGCTCCGAAAGAGACT	1633
QY	1561	CTGCCGAGCTTTTCTTTCTTTTCTCATGTGCCCCGGGAAACAGTCTTTCTTCAGAAATTGT	1620
Db	1634	CTGCCGAGCTTTTCTTTCTTTTCTCATGTGCCCCGGGAAACAGTCTTTCTTCAGAAATTGT	1693
QY	1621	CAGGCTGGGAGGTCAACTTTGTGTGTTCTTTTCCCCCTCACCTGCTTGCCTCTCTTAAAGCCTG	1680
Db	1694	CAGGCTGGGAGGTCAACTTTGTGTGTTCTTTTCCCCCTCACCTGCTTGCCTCTCTTAAAGCCTG	1753
QY	1681	CAGCTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGCACATCCGCTTGTGCCCTTACGCCCTG	1740
Db	1754	CAGCTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGCACATCCGCTTGTGCCCTTACGCCCTG	1813
QY	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGGTCAGGACGCC	1800
Db	1814	TGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGGTCAGGACGCC	1873
QY	1801	TCTGTGTTTGGCACTGGCCCTGATTGTAACCTCTGCCACTTGGGAGAGCTCGGGGTGGT	1860
Db	1874	TCTGTGTTTGGCACTGGCCCTGATTGTAACCTCTGCCACTTGGGAGAGCTCGGGGTGGT	1933
QY	1861	CCCTGGTTTTTCCCTCCTGAGAAATGAGGCGCAGAGGCTCGCTCTCTGAAAGACGCAAGT	1920
Db	1934	CCCTGGTTTTTCCCTCCTGAGAAATGAGGCGCAGAGGCTCGCTCTCTGAAAGACGCAAGT	1993
QY	1921	TGGATGCCACTGGCCTTAGTGTCTGGCCTCACAGCTTCTTGAAGGCTGTCTCAAGGAA	1980
Db	1994	TGGATGCCACTGGCCTTAGTGTCTGGCCTCACAGCTTCTTGAAGGCTGTCTCAAGGAA	2053
QY	1981	AAGACCGCGGCTGGCAACCTTGACATATGCCCTCTTGGGCTCCCTCATCCAGCCCCGTG	2040
Db	2054	AAGACCGCGGCTGGCAACCTTGACATATGCCCTCTTGGGCTCCCTCATCCAGCCCCGTG	2113
QY	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTTGTGTGTTACCCCTCCAGTATT	2100
Db	2114	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTTGTGTGTTACCCCTCCAGTATT	2173
QY	2101	ACCATTTGCCCTCACCTGCGCTTCGTGAGCCCTTTAGTGCAGACAGATGGGGCTGTTT	2160
Db	2174	ACCATTTGCCCTCACCTGCGCTTCGTGAGCCCTTTAGTGCAGACAGATGGGGCTGTTT	2233
QY	2161	TCCCCACCTCTGAGTAGTGTGAGGTCAATACAGAGCTCTTTTTTTTATTGCCCTTTTCT	2220
Db	2234	TCCCCACCTCTGAGTAGTGTGAGGTCAATACAGAGCTCTTTTTTTTATTGCCCTTTTCT	2293
QY	2221	GCCTCTGAATGTTCACTCTGTCCTCTTGTGAGGCGAGGAGGGGTGCCCTCAGG	2280

1862 TCCTGTTTCGCCACTGGCCCTGATTTGAATCTCTGCACCTTGGAGAGAGCTCGGGGTGGT 1921
1861 CCCTGTTTTCCTCTCGAGAGATGAGCGCGAGAGGCTCGCCTCTCTGAAGGACGAGTG 1920
1922 CCCTGTTTTCCTCTCGAGAGATGAGCGCGAGAGGCTCGCCTCTCTGAAGGACGAGTG 1981
1921 TGAATGCACCTGGCTAGTGTCTTGGCTCAACAGCTTCTTGGAGAGCTGTCAAGGAA 1980
1982 TGAATGCACCTGGCTAGTGTCTTGGCTCAACAGCTTCTTGGAGAGCTGTCAAGGAA 2041
1981 AAGCAGCGGCTGGCACTTGGCTCAACAGCTTCTTGGAGAGCTGTCAAGGAGGCTCG 2040
2042 AAGCAGCGGCTGGCACTTGGCTCAACAGCTTCTTGGAGAGCTGTCAAGGAGGCTCG 2101
2041 CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTGTGTGTATACCCCTCCCAAGTAT 2100
2102 CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTGTGTGTATACCCCTCCCAAGTAT 2161
2101 ACCATTTGCCCTCACTGCTTGGTGTAGTGTGAGAGAGAGATGGGGCTGTTT 2160
2162 ACCATTTGCCCTCACTGCTTGGTGTAGTGTGAGAGAGAGATGGGGCTGTTT 2221
2161 TCCCCCACTCTGAGTGTGAGTGTACATACAGCTCTTTTATTTGCTTTTCT 2220
2222 TCCCCCACTCTGAGTGTGAGTGTACATACAGCTCTTTTATTTGCTTTTCT 2281
2221 GCCTCTGAATGTTCACTCTCTGCTCTCTCTTGTGAGGAGAGAGGCTGCTCAAGG 2280
2282 GCCTCTGAATGTTCACTCTCTGCTCTCTCTTGTGAGGAGAGAGGCTGCTCAAGG 2341
2281 GCGGACACTAGTATGATGAGTGTCCAGTGTGAGAGAGAGATTTAAACATGTTGCAACC 2340
2342 GCGGACACTAGTATGATGAGTGTCCAGTGTGAGAGAGAGATTTAAACATGTTGCAACC 2401

RESULT 6

US-10-617-217A-76
; Sequence 76, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
US-10-617-217A-76

Query Match 99.2%; Score 2336.8; DB 16; Length 2401;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATCCTTGGCGCCACAGTCGGGCCACCGGGCTCGCGCGCTCATGAGAGAGCGAGGCGGC 60

Qy

782 ACAGCTTGTGTCAGAGGCGAGGTCGAGCGTCAGGCTCTGGAAGTGTCTGCGCTGGTTT 841
781 TTGGCTTTGACATGTGCAACCTCTTCTTCTTCTTCCGGAAGCAGTATCTGACGCGGC 840
842 TTGGCTTTGACATGTGCAACCTCTTCTTCTTCTTCCGGAAGCAGTATCTGACGCGGC 901
841 AGGAGCGCTCGGCTCAAGCAGATGCAAGAGGAGTTCAGGAGCATGAGGCCAGCTGC 900
902 AGGAGCGCTCGGCTCAAGCAGATGCAAGAGGAGTTCAGGAGCATGAGGCCAGCTGC 961
901 TGAGCGGAGCAAGCCTGAGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
962 TGAGCGGAGCAAGCCTGAGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 1021
961 GCAGCTTCAAGTCTCGGCTTCTTGGAGTGTGGGCACTTGTTCCTGCAACCGAGTCT 1020
1022 GCAGCTTCAAGTCTCGGCTTCTTGGAGTGTGGGCACTTGTTCCTGCAACCGAGTCT 1081
1021 ACCGCGCTTGCAGAGGCCCAAGAGTGCCTTATCTGAGACAGCGGATCACCCGGTGA 1080
1082 ACCGCGCTTGCAGAGGCCCAAGAGTGCCTTATCTGAGACAGCGGATCACCCGGTGA 1141
1081 TACCCCTGTACAAACAGTAAATAGTTTGGAGCGGCACAGCTTGACTGGAAGCACCCTG 1140
1142 TACCCCTGTACAAACAGTAAATAGTTTGGAGCGGCACAGCTTGACTGGAAGCACCCTG 1201
1141 CCCCCTTTTACGGGATTTTATCTCGAGGCTTTTGGAGGAGAGTGTGGGGTGTAGTGT 1200
1202 CCCCCTTTTACGGGATTTTATCTCGAGGCTTTTGGAGGAGAGTGTGGGGTGTAGTGT 1261
1201 CACCTCCAGGATGATGATGAGGAGGAAATGGGTAGAAAATCTTCAGACCCATGCTCCAA 1260
1262 CACCTCCAGGATGATGATGAGGAGGAAATGGGTAGAAAATCTTCAGACCCATGCTCCAA 1321
1261 TGCGAGGATGTGCTTTCACCTCAGAGGAGGACCTGTCTCATGTGCGAGCTCATCAGA 1320
1322 TGCGAGGATGTGCTTTCACCTCAGAGGAGGACCTGTCTCATGTGCGAGCTCATCAGA 1381
1321 GCTCACCTGGGAGATGCGGTGCTCTCTCCAGGAGGAGAGTGTGCGAGTGTG 1380
1382 GCTCACCTGGGAGATGCGGTGCTCTCTCCAGGAGGAGAGTGTGCGAGTGTG 1441
1381 ACTGAAAATGCTCATCACTTAAGCAACAAAGCAGTGTATCAGAGCTCTTCTGTCCTG 1440
1442 ACTGAAAATGCTCATCACTTAAGCAACAAAGCAGTGTATCAGAGCTCTTCTGTCCTG 1501
1441 TGTCTTCTGTTTTTCTGCTGATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1502 TGTCTTCTGTTTTTCTGCTGATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
1501 GCGAGGAAAGCTGGGCGCCGAGTACAAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1562 GCGAGGAAAGCTGGGCGCCGAGTACAAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
1561 CTGCGGAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1620
1622 CTGCGGAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1681
1621 CAGCTGGGAGGTCACCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
1682 CAGCTGGGAGGTCACCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1741
1681 CACGTGTGTAGAGGACAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
1742 CACGTGTGTAGAGGACAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1801
1741 CCGGCGCCCGGCAACAGATTGAAGAGAGATCATGTGAAGGAGAGTGTGTCAGCAGGCC 1800
1802 CCGGCGCCCGGCAACAGATTGAAGAGAGATCATGTGAAGGAGAGTGTGTCAGCAGGCC 1861
1801 TCCTGTTTCGCACTGCGCCCTGATTTGCACTCTCTGCACTTGGAGAGCTCGGGGTGGT 1860

Qy

[illegible]

Db	1142	TACCCCTGTACAACAGCTAATAGTTTTGGAAGCGCACAGCTTGACCTGGAGACACCCCTG	1201
QY	1141	CCCCCTTTTCAGGATTTTATCTCATCAGGCTTTTGAGAGACAGTGGTGGGGGTAGCTGT	1200
Db	1202	CCCCCTTTTCAGGATTTTATCTCGAGGCTTTTGAGGAGACAGTGGTGGGGGTAGCTGT	1261
QY	1201	CACCTCCAGTATGATTGAGGAGGAATTTGGGTAGAAACTCTCCAGACCCATGCCTCCAA	1260
Db	1262	CACCTCCAGTATGATTGAGGAGGAATCGGGTAGAACTCTCCAGACCCATGCCTCCAA	1321
QY	1261	TGGCAGGATGTCCTTTCCCACTGAGAGGGAACCTGTCCATGTGCAGCTCATCAGA	1320
Db	1322	TGGCAGGATGTCCTTTCCCACTGAGAGGGAACCTGTCCATGTGCAGCTCATCAGA	1381
QY	1321	GCCTCACCTGGAGAGATGCGGTGCTCTCCAGAGCCAGATCATGTGCGAGTGTG	1380
Db	1382	GCCTCACCTGGAGAGATGCGGTGCTCTCCAGAGCCAGATCATGTGCGAGTGTG	1441
QY	1381	ACTGAAATGCTCATCACTTAAAGCACCAGGAGGAGTGTGCTGTGGAGTGTG	1440
Db	1442	ACTGAAATGCTCATCACTTAAAGCACCAGGAGGAGTGTGCTGTGGAGTGTG	1501
QY	1441	TGCTCTCTGTTTTTTCTGTTGAATCGTTGTGTGGACTTGGTGGAGACTCAGAG	1500
Db	1502	TGCTCTCTGTTTTTTCTGTTGAATCGTTGTGTGGACTTGGTGGAGACTCAGAG	1561
QY	1501	GGGAGGAAAGCTGGGCCCCAGATACACGAGATGCTTTGGGTGCTCCCTCCAGAGACT	1560
Db	1562	GGGAGGAAAGCTGGGCCCCAGATACACGAGATGCTTTGGGTGCTCCCTCCAGAGACT	1621
QY	1561	CTGCGCGAGCTTTTCTTTTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGCT	1620
Db	1622	CTGCGCGAGCTTTTCTTTTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGCT	1681
QY	1621	CAGGCTGGGAGGTCAACTGTGTCTTTCCCTCAGCTGCTGCTCTTAAAGCCTG	1680
Db	1682	CAGGCTGGGAGGTCAACTGTGTCTTTCCCTCAGCTGCTGCTCTTAAAGCCTG	1741
QY	1681	CAGCTGTGCTAGAGGACAAAAGAGTGAAGTCAGACATCCGCTTCTGCGCAGATGGT	1740
Db	1742	CAGCTGTGCTAGAGGACAAAAGAGTGAAGTCAGACATCCGCTTCTGCGCAGATGGT	1801
QY	1741	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTGGTCAGGACGCCC	1800
Db	1802	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTGGTCAGGACGCCC	1861
QY	1801	TCTGTGTTTCGCACATGGCCCTCATTTGAATCCTGCTCCTTGGGAGAGCTCGGGGTGGT	1860
Db	1862	TCTGTGTTTCGCACATGGCCCTCATTTGAATCCTGCTCCTTGGGAGAGCTCGGGGTGGT	1921
QY	1861	CCCTGTTTTTCCCTCTCTGGAGAAATGAGGCGCAGAGGCTCGCTTCTGAAAGGACGCGAGTG	1920
Db	1922	CCCTGTTTTTCCCTCTCTGGAGAAATGAGGCGCAGAGGCTCGCTTCTGAAAGGACGCGAGTG	1981
QY	1921	TGGATGCCACTGGCTTAGTGTCTGCGCTCACAGCTTCTTGTCAAGAGCTGTCAAGAGAA	1980
Db	1982	TGGATGCCACTGGCTTAGTGTCTGCGCTCACAGCTTCTTGTCAAGAGCTGTCAAGAGAA	2041
QY	1981	AAGCAGCCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2040
Db	2042	AAGCAGCCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2101
QY	2041	CAGCTTTGACATCTTTGGTGTACTCATGTGCGTTCTCTTGTGTACCCCTCCCACTATT	2100
Db	2102	CAGCTTTGACATCTTTGGTGTACTCATGTGCGTTCTCTTGTGTACCCCTCCCACTATT	2161
QY	2101	ACCATTTGCCCTCAGCTGCGCTTGGTAGCCCTTTTAGTGAAGACAGATGGGGCTGTTT	2160
Db	2162	ACCATTTGCCCTCAGCTGCGCTTGGTAGCCCTTTTAGTGAAGACAGATGGGGCTGTTT	2221
QY	2161	TCCCCCAGCTCTGAGTAGTGTGAGGTGCATACACAGCTCTTTTTTATGCGCTTTTCT	2220
Db	2222	TCCCCCAGCTCTGAGTAGTGTGAGGTGCATACACAGCTCTTTTTTATGCGCTTTTCT	2281

QY	1441	TGTCCTCTCTTTTTTTCTGGTGAATCGTTGCTGTGTGCACTTGGTCGAGCACTCAGAG	1501
DB	1502	TGTCCTCTCTTTTTTTCTGGTGAATCGTTGCTGTGTGCACTTGGTCGAGCACTCAGAG	1561
QY	1501	GGGAGGAAAGGCTGGGCCCCGAGTACAACGGATGCTTGGGTGCTGCTCCGAAGAGACT	1560
DB	1562	GGGAGGAAAGGCTGGGCCCCGAGTACAACGGATGCTTGGGTGCTGCTCCGAAGAGACT	1621
QY	1561	CTGCCGCAAGCTTTCTTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT	1620
DB	1622	CTGCCGCAAGCTTTCTTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT	1681
QY	1621	CAGGCTGGGCAAGTCAACTTGTGTTCTTTCTTTCCCTTCACCTGCTGTGCTCTTAAACGCCCTG	1680
DB	1682	CAGGCTGGGCAAGTCAACTTGTGTTCTTTCTTTCCCTTCACCTGCTGTGCTCTTAAACGCCCTG	1741
QY	1681	CACGTGTCTGTAGAGGACAAAGAAAGTGAAGTCAGACATPCGCTTCTGCCAGATGCT	1740
DB	1742	CACGTGTCTGTAGAGGACAAAGAAAGTGAAGTCAGACATPCGCTTCTGCCAGATGCT	1801
QY	1741	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTCAAGGGCAGTTGGTCAGGACGGC	1800
DB	1802	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTCAAGGGCAGTTGGTCAGGACGGC	1861
QY	1801	TCCTGGTTTTCGCCACTGCGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGGT	1860
DB	1862	TCCTGGTTTTCGCCACTGCGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGGT	1921
QY	1861	CCCTGGTTTTCCCTTCGAGAGATGAGGCGCAGAGGCTCGCTCTCTGAAGAACGCAAGTG	1920
DB	1922	CCCTGGTTTTCCCTTCGAGAGATGAGGCGCAGAGGCTCGCTCTCTGAAGAACGCAAGTG	1981
QY	1921	TGGATGCCACTGGCTAGTGTCTCTGGCCCTCACAGCTTCTTGAAGGCTGTCAACAGAA	1980
DB	1982	TGGATGCCACTGGCTAGTGTCTCTGGCCCTCACAGCTTCTTGAAGGCTGTCAACAGAA	2041
QY	1981	AAGCAGCCGCTGGCACTCGAGCATATGCCCTCTTTGGGGCTCCCTCATCCAGGCCGCTCG	2040
DB	2042	AAGCAGCCGCTGGCACTCGAGCATATGCCCTCTTTGGGGCTCCCTCATCCAGGCCGCTCG	2101
QY	2041	CAGCTTTGACATCTGGTGTAAGTCAATGCTGCTTCTCTGTGTTATCCOCTCCCAAGTAT	2100
DB	2102	CAGCTTTGACATCTGGTGTAAGTCAATGCTGCTTCTCTGTGTTATCCOCTCCCAAGTAT	2161
QY	2101	ACCAATTTGCCCTTCACCTGCCCCCTTGCTGAGCCCTTTTAGTGCAAGACAGATGGGGCTGTTT	2160
DB	2162	ACCAATTTGCCCTTCACCTGCCCCCTTGCTGAGCCCTTTTAGTGCAAGACAGATGGGGCTGTTT	2221
QY	2161	TCCCCACCTCTGAGTAGTTGAGGTCACATACAGCTCTTTTTTTTATTGCCCTTTTCT	2220
DB	2222	TCCCCACCTCTGAGTAGTTGAGGTCACATACAGCTCTTTTTTTTATTGCCCTTTTCT	2281
QY	2221	GCCTCTGAATGTTCATCTCTCGTCTCTCTTTGTGAGCGAGGAAGGGTGCCCTCAGGG	2280
DB	2282	GCCTCTGAATGTTCATCTCTCGTCTCTCTTTGTGAGCGAGGAAGGGTGCCCTCAGGG	2341
QY	2281	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2340
DB	2342	GCCGACACTAGTGTGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2401

RESULT 8
US-10-024-298A-74
; Sequence 74, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene

; FILE REFERENCE: 1254-0191P					
; CURRENT APPLICATION NUMBER: US/10/024,298A					
; CURRENT FILING DATE: 2003-04-08					
; PRIOR APPLICATION NUMBER: 60/314,385					
; PRIOR FILING DATE: 2001-08-24					
; PRIOR APPLICATION NUMBER: 60/278,641					
; PRIOR FILING DATE: 2001-03-26					
; PRIOR APPLICATION NUMBER: 60/258,315					
; PRIOR FILING DATE: 2000-12-28					
; PRIOR APPLICATION NUMBER: JP254018/2001					
; PRIOR FILING DATE: 2001-08-24					
; PRIOR APPLICATION NUMBER: JP088912/2001					
; PRIOR FILING DATE: 2001-03-26					
; PRIOR APPLICATION NUMBER: JP402288/2000					
; PRIOR FILING DATE: 2000-12-28					
; NUMBER OF SEQ ID NOS: 182					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO 74					
; LENGTH: 2401					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
; FEATURE:					
; NAME/KEY: CDS					
; LOCATION: (103)..(1158)					
US-10-024-298A-74					

Query Match 99.1%; Score 2335.2; DB 15; Length 2401;					
Best Local Similarity 99.9%; Pred. No. 0;					
Matches 2337; Conservative 0; Mismatches 3; Indels 0; Gaps 0					

QY	1	ATCCTTGGGCGCACAGTCGGCCACCGGGGCTGC	CGCGT	CATGGAGACGAGCGCGCGC	60
Db	62	ATCCTTGGGCGCACAGTCGGCCACCGGGGCTGC	CGCGT	CATGGAGACGAGCGCGCGC	121
QY	61	CTCTGCTGTGCCAGTTCACTCTCTGGCACCACT	CTGTGGT	CACCGCGCCCTGTACT	120
Db	122	CCTCGCTGTGCAGTTCACTCTCTGGCACCACT	CTGTGGT	CACCGCGCCCTGTACT	181
QY	121	CGTGTAACCGCAGAAGSCCGGGTCTCCC	AAGAGCTCA	AGGGAGCTAAAGAGTTCATT	180
Db	182	CGTGTAACCGCAGAAGSCCGGGTCTCCC	AAGAGCTCA	AGGGAGCTAAAGAGTTCATT	241
QY	181	TGGGTGAAGATTTAAAGAGTATCTTT	CAGAAGTCC	CAGGAAAATGGTGCCTTATGCTG	240
Db	242	TGGGTGAAGATTTAAAGAGTATCTTT	CAGAAGTCC	CAGGAAAATGGTGCCTTATGCTG	301
QY	241	TTATAGAAGGAGCTGCGGTCTGTTAA	GAAAGCCTT	AACAGCAGCTTTGTGAAAACT	300
Db	302	TTATAGAAGGAGCTGCGGTCTGTTAA	GAAAGCCTT	AACAGCAGCTTTGTGAAAACT	361
QY	301	GCAAGGGGTAAATTCAGCGGCTGACA	CTTCAGGAGCA	CAAGATGGTGTGGAATCGAACCA	360
Db	362	GCAAGGGGTAAATTCAGCGGCTGACA	CTTCAGGAGCA	CAAGATGGTGTGGAATCGAACCA	421
QY	361	CCACCTTTGGAATGATTTGCTCAA	GATCATTT	CATCAGAGGACCAACACAGTGCCTTTG	420
Db	422	CCACCTTTGGAATGATTTGCTCAA	GATCATTT	CATCAGAGGACCAACACAGTGCCTTTG	481
QY	421	ACCTGTGCCCCACGAGGATGGCGT	GGATGGCT	GTGCGAGTGTGAAGCCCTGTGACT	480
Db	482	ACCTGTGCCCCACGAGGATGGCGT	GGATGGCT	GTGCGAGTGTGAAGCCCTGTGACT	541
QY	481	CAGTGGATCTGGGTCTAGAGACT	TGTTATG	AAGATTTCCACCCTCGATTTCAGTCTCTTCA	540
Db	542	CAGTGGATCTGGGTCTAGAGACT	TGTTATG	AAGATTTCCACCCTCGATTTCAGTCTCTTCA	601
QY	541	CCGATCTATCGGCCACTACATCAG	CGGTGAG	CGGCCCAAGGCAATCCAAGAGACCGAGG	600
Db	602	CCGATCTATCGGCCACTACATCAG	CGGTGAG	CGGCCCAAGGCAATCCAAGAGACCGAGG	661
QY	601	AGATGCTGAAGTGGGGGCCACCCCT	CACAGGGGTTGGCGAA	CTGGTCTGGHCAACAACACT	660
Db	662	AGATGCTGAAGTGGGGGCCACCCCT	CACAGGGGTTGGCGAA	CTGGTCTGGHCAACAACACT	721

Qy	1741	CGGGCCCCGGGCAACAGATATGAAGAGAGATCATGTGAAGGCAGTGTGGTCAGCAGGCC	1800
Db	1802	CGGGCCCCGGGCAACAGATATGAAGAGAGATCATGTGAAGGCAGTGTGGTCAGCAGGCC	1861
Qy	1801	TCCTGGTTTCGCACATGGCCCTGATTTGAACCTCTGCACACTTGGGAGAGCTCGGGGTGGT	1860
Db	1862	TCCTGGTTTCGCACATGGCCCTGATTTGAACCTCTGCACACTTGGGAGAGCTCGGGGTGGT	1921
Qy	1861	CCCTGGTTTTCCTCTCTGGAGAAATGAGGGCGAGAGCCTCGCCTCTCTGAAGACGCAGTG	1920
Db	1922	CCCTGGTTTTCCTCTCTGGAGAAATGAGGGCGAGAGCCTCGCCTCTCTGAAGACGCAGTG	1981
Qy	1921	TGGATGCCACTGGCCTAGTGTCTCTGGCCTCACAGCTTCCTTCAGAGGCGTGTACAAAGAA	1980
Db	1982	TGGATGCCACTGGCCTAGTGTCTCTGGCCTCACAGCTTCCTTCAGAGGCGTGTACAAAGAA	2041
Qy	1991	AAGCAGCGGCTGGCACCTCGACATGCGCCTCTTGGGGCTCCCTCATCCAGCCCGTGG	2040
Db	2042	AAGCAGCGGCTGGCACCTCGACATGCGCCTCTTGGGGCTCCCTCATCCAGCCCGTGG	2101
Qy	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTCTGTGTATACCCCTCCAGTATT	2100
Db	2102	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTCTGTGTATACCCCTCCAGTATT	2161
Qy	2101	ACCATTTGCCCTCACCTGCCCTTGTGAGCCTTTAGTGCAGACAGATGGGGCTGTATT	2160
Db	2162	ACCATTTGCCCTCACCTGCCCTTGTGAGCCTTTAGTGCAGACAGATGGGGCTGTATT	2221
Qy	2161	TCCCCACCTCTGAGTAGTTGGAGGTACACATACAGCTCTTTTTTTATTGCCCTTTTCT	2220
Db	2222	TCCCCACCTCTGAGTAGTTGGAGGTACACATACAGCTCTTTTTTTATTGCCCTTTTCT	2281
Qy	2221	GGCTCTGAATGTCATCTCTGTCCTCTTTGTGCGGAGGAAGGGGTGCCCTCAGGG	2280
Db	2282	GGCTCTGAATGTCATCTCTGTCCTCTTTGTGCGGAGGAAGGGGTGCCCTCAGGG	2341
Qy	2281	GGCGACATAGTATGATGCAGTGTGCAGTGTGAACACAGAAAAATTAACATGTGTCAACC	2340
Db	2342	GGCGACATAGTATGATGCAGTGTGCAGTGTGAACACAGAAATTAACATGTGTCAACC	2401

RESULT 9

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US-10-042-211A-74
; Sequence 74, Application US/10042211A
; Publication No. US20030170719A1
;
; GENERAL INFORMATION:
;
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE OF INVENTION: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/259,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
;
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
;
US-10-042-211A-74

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QY	661	CTGTCCGCTCGAGCGCCCAACAAAGGCATCAGTACTATCTAAGACGCCAGGACTTCG	720
DB	722	CTGTCCGCTCGAGCGCCCAACAAAGGCATCAGTACTATCTAAGACGCCAGGACTTCG	781
QY	721	ACAGCCTGTGACAGGCGAGGAGTCGAGCGTCAGGCTCTGGAGGTGCTGGCGCTGGTT	780
DB	782	ACAGCCTGTGACAGGCGAGGAGTCGAGCGTCAGGCTCTGGAGGTGCTGGCGCTGGTT	841
QY	781	TTGGCTTTGCCACATGTGCGCCCTCTTCTTCAATTCCTCGGAAGCAGTATCTGACGGC	840
DB	842	TTGGCTTTGCCACATGTGCGCCCTCTTCTTCAATTCCTCGGAAGCAGTATCTGACGGC	901
QY	841	AGGAGCGCTGCGCCTCAAGCAGATCGAGGAGAGTCTCAGGAGCATGAGGCCAGCTGC	900
DB	902	AGGAGCGCTGCGCCTCAAGCAGATCGAGGAGAGTCTCAGGAGCATGAGGCCAGCTGC	961
QY	901	TCGAGCGAGCAGGCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA	960
DB	962	TGAGCCGAGCCAAAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA	1021
QY	961	GCAGCTTCAAGTCCTGCGTCTTCTTGAGTGTGGGACGTTTGTCTCTGACCGAGTGCT	1020
DB	1022	GCAGCTTCAAGTCCTGCGTCTTCTTGAGTGTGGGACGTTTGTCTCTGACCGAGTGCT	1081
QY	1021	ACGGCGCTGCCAGAGCCCAAGAGTGCCTATCTCCAGACAGGCGCATACCCGGGTGA	1080
DB	1082	ACGGCGCTGCCAGAGCCCAAGAGTGCCTATCTCCAGACAGGCGCATACCCGGGTGA	1141
QY	1081	TACCCCTGTACAAACAGCTAATAGTTTGGAAAGCCGACAGCTTGAAGCAGCCCTG	1140
DB	1142	TACCCCGGTACAAACAGCTAATAGTTTGGAAAGCCGACAGCTTGAAGCAGCCCTG	1201
QY	1141	CCCGCTTTGAGGATTTTATCTCGAGGCTTTGGAGGACGAGTGTGGGGTAGCTGT	1200
DB	1202	CCCGCTTTGAGGATTTTATCTCGAGGCTTTGGAGGACGAGTGTGGGGTAGCTGT	1261
QY	1201	CACCTCCAGGTATGATTTGAGGAGGAATGGGTAGAACTCTCCAGACCCATGCTCCAA	1260
DB	1262	CACCTCCAGGTATGATTTGAGGAGGAATGGGTAGAACTCTCCAGACCCATGCTCCAA	1321
QY	1261	TGGCAGGATGTGCTTTTCCACCTGAGAGGGACCTGTCCATGTGCAGCCTCATCAGA	1320
DB	1322	TGGCAGGATGTGCTTTTCCACCTGAGAGGGACCTGTCCATGTGCAGCCTCATCAGA	1381
QY	1321	GCCTCACCTGGAGGATGCGTGGCGTCTCTCCAGGAGCCAGATCAGTGCAGTGTG	1380
DB	1382	GCCTCACCTGGAGGATGCGTGGCGTCTCTCTCCAGGAGCCAGATCAGTGCAGTGTG	1441
QY	1381	ACTGAAATGCTCATCTTAAGCACAAAGCCAGTGATCAGAGCTCTTCTGTCTCTG	1440
DB	1442	ACTGAAATGCTCATCTTAAGCACAAAGCCAGTGATCAGAGCTCTTCTGTCTCTG	1501
QY	1441	TGCTCTCTGTTTTTCTGGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1500
DB	1502	TGCTCTCTGTTTTTCTGGTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1561
QY	1501	GGGAGGAAAGGCTGGGCCCCGAGTACAAAGGATGCTTGGGTGTGCTCTCGAAGAGCT	1560
DB	1562	GGGAGGAAAGGCTGGGCCCCGAGTACAAAGGATGCTTGGGTGTGCTCTCGAAGAGCT	1621
QY	1561	CTGCGCGAGCTTTCTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAATTGT	1620
DB	1622	CTGCGCGAGCTTTCTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAATTGT	1681
QY	1621	CAGGCTGGGAGGTAACCTTGTCTCTTTTCCCTCACTGTGTGCTCTTAAACGCTG	1680
DB	1682	CAGGCTGGGAGGTAACCTTGTCTCTTTTCCCTCACTGTGTGCTCTTAAACGCTG	1741
QY	1681	CACGTGTGTAGAGGACAAAGAGTGAAGTACACATCCGCTTCTGCCAGATGGT	1740
DB	1742	CACGTGTGTAGAGGACAAAGAGTGAAGTACACATCCGCTTCTGCCAGATGGT	1801

Query Match									
Best Local Similarity 99.1%; Score 2335.2; DB 15; Length 2401;									
Matches 2337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	ATCCTGGCGCCACAGCTCGGCACACCGGGGCTGCGCCCTCATGAGAGCGGAGCGCGC	60						
DB	62	ATCCTTTGGCGCCACAGTCGCGCCACCGGGGCTGCGCCCTCATGAGAGCGGAGCGCGC	121						
QY	61	CCTCGCTGTGCCAGTTTCATCTCTCTGGGCACACACTCTGTGTGTCAACCGCCCTGTACT	120						
DB	122	CCTCGCTGTGCCAGTTTCATCTCTCTGGGCACACACTCTGTGTGTCAACCGCCCTGTACT	181						
QY	121	CGTGTACCGGCAGAGAGCGCGGCTCTCCAGAGCTCAAGGGAGCTAAAAAGTTCAAT	180						
DB	182	CGTGTACCGGCAGAGAGCGCGGCTCTCCAGAGCTCAAGGGAGCTAAAAAGTTCAAT	241						
QY	181	TGGGTGAAGATTAAAGATATTCTTTCAAGAGCTCCAGGAAATGCGTGTCTTANGCTG	240						
DB	242	TGGGTGAAGATTAAAGATATTCTTTCAAGAGCTCCAGGAAATGCGTGTCTTANGCTG	301						
QY	241	TTATGAAGAGAGCTGTGCGGTCTGTATAAGAAACGCTTAAAGCCAGTTGTGNAAACT	300						
DB	302	TTATGAAGAGAGCTGTGCGGTCTGTATAAGAAACGCTTAAAGCCAGTTGTGNAAACT	361						
QY	301	GCAAGGGGTAAATCAGCGGCTGACACTTTCAGGAGCAACAAGATGGTGTGGAATCGAACCA	360						
DB	362	GCAAGGGGTAAATCAGCGGCTGACACTTTCAGGAGCAACAAGATGGTGTGGAATCGAACCA	421						
QY	361	CCCACCTTTGGAAATGCTCAAGATCATTTATCAGAGACCAACACAGTGCCTTTTG	420						
DB	422	CCCACCTTTGGAAATGCTCAAGATCATTTATCAGAGACCAACACAGTGCCTTTTG	481						
QY	421	ACCTGGTCCCCACAGAGATGGCGTGGATGTGGCTGTGCGAGTCTGAGGCCCTGGACT	480						
DB	482	ACCTGGTCCCCACAGAGATGGCGTGGATGTGGCTGTGCGAGTCTGAGGCCCTGGACT	541						
QY	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGAATCAGTCCTTCA	540						
DB	542	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGAATCAGTCCTTCA	601						
QY	541	CCGATGTATCGGCACCTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGACCGAGG	600						
DB	602	CCGATGTATCGGCACCTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGACCGAGG	661						
QY	601	AGATGCTGAAGGTGGGGGCCACCCCTCAAGGGGTGGCGAAGTGGTCTCTGGAACAACACT	660						
DB	662	AGATGCTGAAGGTGGGGGCCACCCCTCAAGGGGTGGCGAAGTGGTCTCTGGAACAACACT	721						
QY	661	CTGTCCGCTCAGCGCGCCCAACAGGCGATGCGTACTATCTAAGCAGCAGGACTTCG	720						
DB	722	CTGTCCGCTCAGCGCGCCCAACAGGCGATGCGTACTATCTAAGCAGCAGGACTTCG	781						
QY	721	ACAGCTGTGCGAGCAGAGTCGAGCTCAGGCTCGAAGAGTGTGCGCGCTGGTTT	780						
DB	782	ACAGCTGTGCGAGCAGAGTCGAGCTCAGGCTCGAAGAGTGTGCGCGCTGGTTT	841						
QY	781	TTGCGCTTTGCCACATGTGCCACCTCTTCTTCAATTTCTCCGGAAGCAGTATCTGACGCGC	840						
DB	842	TTGCGCTTTGCCACATGTGCCACCTCTTCTTCAATTTCTCCGGAAGCAGTATCTGACGCGC	901						
QY	841	AGAGCGCCTGCGCCTCAAGCAGATCAGGAGGAGTTCCAGGAGCATGAGGCCACAGCTGC	900						
DB	902	AGAGCGCCTGCGCCTCAAGCAGATCAGGAGGAGTTCCAGGAGCATGAGGCCACAGCTGC	961						
QY	901	TGAGCCGAGCCAGCCTGAGCAGAGGAGTCTGAAGAGCGCCTGTGTAGTGTCTGA	960						
DB	962	TGAGCCGAGCCAGCCTGAGCAGAGGAGTCTGAAGAGCGCCTGTGTAGTGTCTGA	1021						
QY	961	GCAGCTTCAAGTCTCTGCTTTCTGAGTGTGGGCACGTTTGTCTCTGACCGAGTGTCT	1020						
DB	1022	GCAGCTTCAAGTCTCTGCTTTCTGAGTGTGGGCACGTTTGTCTCTGACCGAGTGTCT	1081						
QY	1021	ACCGCGCTTCCACAGAGCCCAAGAGTGCCTATCTTCAGACAGCGCGATCACCCGGGTGA	1080						
DB	1082	ACCGCGCTTCCACAGAGCCCAAGAGTGCCTATCTTCAGACAGCGCGATCACCCGGGTGA	1141						
QY	1081	TACCCCTGTACAAACAGCTTAATAGTTTGGAGCGCGCACAGCTTGACCTTGGAGACACCCCTG	1140						
DB	1142	TACCCCTGTACAAACAGCTTAATAGTTTGGAGCGCGCACAGCTTGACCTTGGAGACACCCCTG	1201						
QY	1141	CCCCTTTTTCAGGGAATTTTATCTCGAGGCGCTTTTGGAGGACAGTGTGTGGGGGTAGCTGT	1200						
DB	1202	CCCCTTTTTCAGGGAATTTTATCTCGAGGCGCTTTTGGAGGACAGTGTGTGGGGGTAGCTGT	1261						
QY	1201	CACCTCAGATATGATTGAGGGAGGAATTGGGTAGAAAATCTCCACACCCATGCCTCCAA	1260						
DB	1262	CACCTCAGATATGATTGAGGGAGGAATCGGGTAGAAAATCTCCACACCCATGCCTCCAA	1321						
QY	1261	TGGCAGGATCTGCTTTTCCACCTCAGAGGGGACCTGTCCATGTGCGACCTCATCAGA	1320						
DB	1322	TGGCAGGATCTGCTTTTCCACCTCAGAGGGGACCTGTCCATGTGCGACCTCATCAGA	1381						
QY	1321	GCCTCACTCTGGAGGATGCGCGTGTGGCGTCTCTCCAGAGGACAGATCAGTGCAGGTGTG	1380						
DB	1382	GCCTCACTCTGGAGGATGCGCGTGTGGCGTCTCTCCAGAGGACAGATCAGTGCAGGTGTG	1441						
QY	1381	ACTGAAATGCCTCATCATTTAAGCAACAAAGCCAGTGATCAGCAGCTCTTCTGTTCCTG	1440						
DB	1442	ACTGAAATGCCTCATCATTTAAGCAACAAAGCCAGTGATCAGCAGCTCTTCTGTTCCTG	1501						
QY	1441	TGTCTTCTGTTTTTCTCGTGAATCGTTGCTTGTGTGGACTTGGTGGAGACTCAGAG	1500						
DB	1502	TGTCTTCTGTTTTTCTCGTGAATCGTTGCTTGTGTGGACTTGGTGGAGACTCAGAG	1561						
QY	1501	GGAGGAAAGGCTGGGCCCGCGAGTACAACGGATGCTTGGGTGCTGCCCTCCAGAGACT	1560						
DB	1562	GGAGGAAAGGCTGGGCCCGCGAGTACAACGGATGCTTGGGTGCTGCCCTCCAGAGACT	1621						
QY	1561	CTGCGCAGCTTTTCTTCTTTTCTCATGCCCGGGAAACAGTCTTTTTCAGAAATGT	1620						
DB	1622	CTGCGCAGCTTTTCTTCTTTTCTCATGCCCGGGAAACAGTCTTTTTCAGAAATGT	1681						
QY	1621	CAGGCTGGCGAGCTCAACTTGTGTCTTTTCCCTCAGCTGCTGCTTAAAGCGCTG	1680						
DB	1682	CAGGCTGGCGAGCTCAACTTGTGTCTTTTCCCTCAGCTGCTGCTTAAAGCGCTG	1741						
QY	1681	CACTGTGTGTAGAGGCAAAAAGAGTGAAGTCAAGCATCCGCTTCTGCCAGATGGT	1740						
DB	1742	CACGTGTGTGTAGAGGCAAAAAGAGTGAAGTCAAGCATCCGCTTCTGCCAGATGGT	1801						
QY	1741	CGGGGCCCGGGCAACAGATTGAAGAGATCATGTGAAGGGCAGTGGTCAAGCAGGCC	1800						
DB	1802	CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTGGTCAAGCAGGCC	1861						
QY	1801	TCTGCTTTTCCCTCCTGCGCCCTGATTTGAACTCTGCCACCTGGGAGAGCTCGGGGTGGT	1860						
DB	1862	TCTGCTTTTCCCTCCTGCGCCCTGATTTGAACTCTGCCACCTGGGAGAGCTCGGGGTGGT	1921						
QY	1861	CCCTGGTTTTTCCCTCCTGGAGAATGAGCGCGCAGAGGCTCGCTCTCTGAAGAGCGCAGTG	1920						
DB	1922	CCCTGGTTTTTCCCTCCTGGAGAATGAGCGCGCAGAGGCTCGCTCTCTGAAGAGCGCAGTG	1981						
QY	1921	TGGATGCCACTTGGCCTTAGTGTCTGGCCTCAAGCTTCTTTCGAAGGCTGTCACAAGGAA	1980						
DB	1982	TGGATGCCACTTGGCCTTAGTGTCTGGCCTCAAGCTTCTTTCGAAGGCTGTCACAAGGAA	2041						
QY	1981	AAGCAGCGCGCTGCGCCCTCAGCATATGCCCTCTTGGGGCTCCCTCATTCAGGCCCTGCG	2040						
DB	2042	AAGCAGCGCGCTGCGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATTCAGGCCCTGCG	2101						
QY	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTCTGTGTGTGTGTGTGTGTGTGTGT	2100						
DB	2102	CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTCTGTGTGTGTGTGTGTGTGTGTGT	2161						
QY	2101	ACCAATTTGCCCTCAGCTGCCCTTGTGTGAGGCTTTTAGTGCAAAGACAGATGGGGCTGT	2160						


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1442 ACTGAAATGCCTCATCACTTAAGACCAAAAGCCAGTGATCAGCAGCTCTCTGTCCTG 1501
1441 TGTCTTCTGTTTTTCTGTTGATCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1502 TGTCTTCTGTTTTTCTGTTGATCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
1501 GGGAGAAAGGCTGGGCCCCGAGTACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1560
1562 GGGAGAAAGGCTGGGCCCCGAGTACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1621
1561 CTGCCCCAGCTTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
1622 CTGCCCCAGCTTTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1681
1621 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
1682 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1741
1681 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
1742 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1801
1741 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
1802 CAGGCTGGGAGCTCAACTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1861
1801 TCTGTTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
1862 TCTGTTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1921
1861 CCGTGGTTTCCCTCCTGAGAAATGAGCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1920
1922 CCGTGGTTTCCCTCCTGAGAAATGAGCGCAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1981
1921 TGGATGCCACTGGCCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
1982 TGGATGCCACTGGCCTAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2041
1981 AAGCAGCGCGCTGGCAGCTGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
2042 AAGCAGCGCGCTGGCAGCTGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2101
2041 CAGCTTTGACATCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2102 CAGCTTTGACATCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2161
2101 ACCATTTGCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2162 ACCATTTGCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
2161 TCCCTCCACCTCTGAGTAGTTGGAGGTCACATACAGCTCTTTTATTTGCTGCTTTCT 2220
2222 TCCCTCCACCTCTGAGTAGTTGGAGGTCACATACAGCTCTTTTATTTGCTGCTTTCT 2281
2221 GCTCTGAATGTTTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2282 GCTCTGAATGTTTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2341
2281 GCGGACACTAGTAGTATGAGTGTCCAGTGTGAACAGCAGAAATTTAAACATGTTGCAACC 2340
2342 GCGGACACTAGTAGTATGAGTGTCCAGTGTGAACAGCAGAAATTTAAACATGTTGCAACC 2401

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RESULT 11

US-10-024-298A-74

; Sequence 74, Application US/10024298A

; Publication No. US20040214167A9

; GENERAL INFORMATION:

; APPLICANT: ASHAI KASEI KABUSHIKI KAISHA

; APPLICANT: AKIO MATSUDA

; APPLICANT: GOICHI HONDA

; APPLICANT: SHUJI MURAMATSU

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; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP008912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 74
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
; US-10-024-298A-74

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Query Match

Best Local Similarity 99.1%; Score 2335.2; DB 18; Length 2401;

Matches 2337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATCTTGGCGCCACAGTCGGCCACCGCGGCTCGCGCGCTCATGAGAGCGAGCGGCGGC 60
DB 62 ATCTTGGCGCCACAGTCGGCCACCGCGGCTCGCGCGCTCATGAGAGCGAGCGGCGGC 121
QY 61 CCTGCTGTGCGAGTTATCTCTCTGCGSCACCACTCTGTGCTCACCCCGCCCTTACT 120
DB 122 CCTGCTGTGCGAGTTATCTCTCTGCGSCACCACTCTGTGCTCACCCCGCCCTTACT 181
QY 121 CCGGTACCGGCACAAAGCGCGGCTCTCCAAAGAGCTCAAGGAGCTAAAAAGTTTATT 180
DB 182 CCGGTACCGGCACAAAGCGCGGCTCTCCAAAGAGCTCAAGGAGCTAAAAAGTTTATT 241
QY 181 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCTGCTTATGCTG 240
DB 242 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCTGCTTATGCTG 301
QY 241 TTATAGAAGAGCTGTGCGGTCTGTTTAAAGAAAGCGCTTAAACAGCAGTTTGTGAAAACT 300
DB 302 TTATAGAAGAGCTGTGCGGTCTGTTTAAAGAAAGCGCTTAAACAGCAGTTTGTGAAAACT 361
QY 301 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGAGGACCAAGATGTTGGAATCGAAACCA 360
DB 362 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGAGGACCAAGATGTTGGAATCGAAACCA 421
QY 361 CCCACCTTTTGAATGATTTGCTCAAAGATCATTCATCAGAGGACCAACAGATGCGCTTTG 420
DB 422 CCCACCTTTTGAATGATTTGCTCAAAGATCATTCATCAGAGGACCAACAGATGCGCTTTG 481
QY 421 ACTGTGTGCCCCACAGAGGATGCGGTGATGTTGCTGTGCGAGTGTGGAAGCCCTGAGCT 480
DB 482 ACTGTGTGCCCCACAGAGGATGCGGTGATGTTGCTGTGCGAGTGTGGAAGCCCTGAGCT 541
QY 481 CAGTGTGATCTGGGTCTTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCCTTCA 540
DB 542 CAGTGTGATCTGGGTCTTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCCTTCA 601
QY 541 CCGATGTATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGGAG 600
DB 602 CCGATGTATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGGAG 661
QY 601 AGATGCTGAAGGTGGGGGCCACCCCTCACAGGGGTTGGCGAATGCTGCTCGGACAACT 660

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1742 CACGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACATCCGCTTCTGCCACGATGGT 1801
1741 CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGAGGAGTGGTTCAGCAGGCC 1800
1802 CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGAGGAGTGGTTCAGCAGGCC 1861
1801 TCCTGGTTTCGCCCATCGCCCTGATTTGAACCTCTGCACTTGGGAGAGCTCGGGGTGGT 1860
1862 TCCTGGTTTCGCCCATCGCCCTGATTTGAACCTCTGCACTTGGGAGAGCTCGGGGTGGT 1921
1861 CCCTGGTTTCGCCCATCGCCCTGATTTGAACCTCTGCACTTGGGAGAGCTCGGGGTGGT 1920
1922 CCCTGGTTTCGCCCATCGCCCTGATTTGAACCTCTGCACTTGGGAGAGCTCGGGGTGGT 1981
1921 TGGATGCCACTGGCTAGTGTCTGCTGCTCAGAGCTTCTTTCGCAAGGCTGTCAAGGAA 1980
1982 TGGATGCCACTGGCTAGTGTCTGCTGCTCAGAGCTTCTTTCGCAAGGCTGTCAAGGAA 2041
1981 AAGCAGCCGGCTGGCACCCTGAGCATATGCCCCTCTTGGGGCTCCCTCATCCAGCCCTCG 2040
2042 AAGCAGCCGGCTGGCACCCTGAGCATATGCCCCTCTTGGGGCTCCCTCATCCAGCCCTCG 2101
2041 CAGCTTTCAGATCTTGGTGTACTCATGTCTGCTTCTCTTGTGTGTTACCCCTCCCAAGTAT 2100
2102 CAGCTTTCAGATCTTGGTGTACTCATGTCTGCTTCTCTTGTGTGTTACCCCTCCCAAGTAT 2161
2101 ACCATTGGCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2162 ACCATTGGCCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2221
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2222 TCCCCCAGCTCTGAGTAGTGGAGTCAATACAGCTCTTTTATTTATTTGCTTTTCT 2281
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2282 GCCTCTGAATGTTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2341
2281 GCCGACACTAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2342 GCCGACACTAGTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2401

RESULT 12
US-09-764-864-14
; Sequence 14, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2446
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-864-14

Query Match 98.9%; Score 2330.8; DB 9; Length 2446;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 3; Mismatches 0; Indels 2; Gaps 2;
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Db 82 ATCCTTGGCCCAAGTTCGGCCACCGGGGCTCGCCGCCCTCATGAGAGCGGAGCGGCGC 141
Qy 61 CCTCGCTGTGCGAGTTTCATCTCTGCTGGGCAACCTCTGTGTGTCAACCGCCCTGTACT 120
Db 142 CCTCGCTGTGCGAGTTTCATCTCTGCTGGGCAACCTCTGTGTGTCAACCGCCCTGTACT 201

662 AGATGCTGAAGGTGGGGCCACCTCTACAGGGGTGGCGAATCGTCTCTGCAACAACACT 721
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722 CTGTCCGCTGTCAGCGCCGCCAAACAGGATGAGTACTATCTAAGAGAGCCAGGACTTCG 781
721 ACAGCTTGTCTCAGAGGAGGAGTTCGAGCGTCAAGCTCTGGAAGGTGCTGGCGTGGTTT 780
782 ACAGCTTGTCTCAGAGGAGGAGTTCGAGCGTCAAGCTCTGGAAGGTGCTGGCGTGGTTT 841
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841 AGGAGCGCTGGCTCAGAGAGTTCAGAGGAGTTCAGAGCATGAGGCGCCAGCTTCG 900
902 AGGAGCGCTGGCTCAGAGAGTTCAGAGGAGTTCAGAGCATGAGGCGCCAGCTTCG 961
901 TGAGCCGAGCCAAAGCTTCAGAGAGTTCAGAGGAGTTCAGAGCGCTGTGTGTGTGTCTGA 960
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DB 262 TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATCGTGCCTTATGCTG 321
QY 241 TTATAGAAGGAGCTGCGGTCTGTTTAAAGAAACGCTTAAAGCCAGTTTGTGGAACCT 300
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DB 382 GCAAGGGGTAAATTCAGCGGCTGACATTCAGAGCACAAAGATGGTGTGGAATCGAACCA 441
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DB 1881 TCCTGTTTTCGCACTGSCCTGATTTGAACTCTGCTGCTGCTGAGAGCTGCGGGTGT 1940
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DB 1941 CCCTGTTTTCCTCTCGAGAGATGAGCGCGAGAGGCTTCGCTTCTGAAAGAGCAGATG 2000
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DB 2001 TGGATGCCACTGGCCTAGTGTCTTGGCTTCAAGCTTCTTGAAGGCTGTCAAGAGAA 2060
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QY 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTGTTTACCCCTCCAGATTT 2100
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QY 2281 GCGCACACTAGTATGATGAGTGTCCAGTGTGAACAGACAGAAATTAACATGTTGCAAC 2340

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 20:08:22 ; Search time 1047 Seconds
(without alignments)
11812.451 Million cell updates/sec

Title: US-09-978-360A-32
Perfect score: 2356
Sequence: 1 atccctggcgcacagtcgg.....aaccaaaaaaaaaaaaaa 2356

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	100.0	2356	3	AA87756 Human sec
2	2356	100.0	2356	5	AA64038 cDNA enco
3	2356	100.0	2356	12	ADP18776 Human sec
4	2338.4	99.3	2413	4	AD12597 Human pro
5	2336.8	99.2	2401	6	ABQ91949 Human NF-
6	2335.2	99.1	2401	6	ABQ91948 Human NF-
7	2332	99.0	2442	4	AAH16130 Human cDN
8	2330.8	98.9	2431	4	AA502044 DNA enco
9	2330.8	98.9	2446	4	AA525835 Human cDN
10	2330.8	98.9	2446	8	ABX73176 Human nov
11	2291.8	97.3	2717	6	ABN59817 Novel hum
12	2217	94.1	2377	5	ABA82998 Human tra
13	1907.4	81.0	2080	8	ABT42547 Human nuc
14	1766	75.0	1791	4	AA526296 Human cDN
15	1766	75.0	1791	8	ABX73637 Human nov
16	1751.4	74.3	1780	6	ABL90713 Human pol
17	476.6	20.2	512	4	AAH11159 Human cDN
18	435	18.5	435	10	AA59606 Human gen
19	363	15.4	374	6	ABL66011 Lung canc
20	338.8	14.4	484	4	AAH06088 Human cDN
21	309	13.1	343	2	AA51937 Human sec

22	307.4	13.0	378	2	AA40363
23	304.6	12.9	391	2	AA40593
24	290.8	12.3	398	8	ABX5547
25	124.6	5.3	197	2	AA40327
26	95.6	4.1	1086	4	ABL2113
27	74.6	3.2	3475	4	ABL2112
28	65.2	2.8	5019	4	ABL26430
29	60.6	2.6	4086	4	ABL26430
30	60	2.5	60	6	ABN40374
31	58.6	2.5	2000	8	ADA71938
32	53.4	2.3	2000	8	ADA71938
33	51	2.2	51	4	AAI78808
34	49.4	2.1	51	4	AAI78809
35	45.8	1.9	1239	9	ACF06126
36	45.8	1.9	4356	2	AAQ37543
37	45.6	1.9	4161	4	ABL09363
38	45.6	1.9	24066	4	ABL09362
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43	43.2	1.8	1227	2	AAV84121
44	42.8	1.8	1716	12	ADJ40227
45	42.8	1.8	1782	8	ADA71107

ALIGNMENTS

RESULT 1
AA87756
ID AAA87756 standard; cDNA; 2356 BP.
AC AAA87756;
XX
DT 28-NOV-2000 (first entry)
XX
DE Human secreted protein encoding cDNA SEQ ID #55.
XX
KW Human; secreted protein; forensic procedure; gene therapy;
KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondrial cytopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; ss.
XX
OS Homo sapiens.
XX
PN WO200037491-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-IB002058.
XX
PR 22-DEC-1998; 98US-0113686P.
XX
PR 25-JUN-1999; 99US-0141032P.
XX
(GEST) GENSET.
XX
Bougueleret L, Dumas J, Duclert A;
XX
WPI; 2000-442637/38.
XX
P-PSDB; AAB25794.
XX
Polynucleotides and polypeptides encoding proteins with signal peptides,
XX
useful in diagnostic, forensic, gene therapy and chromosome mapping
XX
procedures.
XX
Claim 1; Page 218-220; 306pp; English.
XX
This sequence represents human cDNA encoding a secreted protein. The
XX
invention relates to sequences AAA87755-AA87774 which encode human

secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy, and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidemia, septic shock and impotence

XX
SQ Sequence 2356 BP; 494 A; 651 C; 665 G; 546 T; 0 U; 0 Other;

Query Match 100.0%; Score 2356; DB 3; Length 2356;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTCTGCTGTCGAGTTTCATCTCTCTGGGACCACTCTGTGGTCAACCGCGCCCTTACT 120
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QY 481 CAGTGGATCTGGGCTTAGAGACTGTGTATGAGAAAGTTCCACCCCTGATTCAGTCTCA 540
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901 TGAGCCGAGCCAGACCTGAGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
 961 GCAGCTTCAAGTCTGCTGCTTTCTGAGTGTGGGACAGTTTGTCTGACCCAGTGTCT 1020
 961 GCAGCTTCAAGTCTGCTGCTTTCTGAGTGTGGGACAGTTTGTCTGACCCAGTGTCT 1020
 1021 ACCGCGCTTCCAGAGCCCAAGAGTGCCTATCTGAGACAGGCGCATCAACCCGGGTGA 1080
 1021 ACCGCGCTTCCAGAGCCCAAGAGTGCCTATCTGAGACAGGCGCATCAACCCGGGTGA 1080
 1081 TACCCCTGTGA CAACAGCTAATAGTTGAAGCCGACAGCTTGACCTGGAAGCACCCCTG 1140
 1081 TACCCCTGTGA CAACAGCTAATAGTTGAAGCCGACAGCTTGACCTGGAAGCACCCCTG 1140
 1141 CCCCTTTTCAAGGATTTTATCTGAGCGCTTTTGGAGGAGCAGTGTGGGGGTAGCTGT 1200
 1141 CCCCTTTTCAAGGATTTTATCTGAGCGCTTTTGGAGGAGCAGTGTGGGGGTAGCTGT 1200
 1201 CACCTCCAGGTATGATGAGGAGGAATTTGGGTGAAACTCTCCAGACCCATGCCCTCAA 1260
 1201 CACCTCCAGGTATGATGAGGAGGAATTTGGGTGAAACTCTCCAGACCCATGCCCTCAA 1260
 1261 TGGAGGATGTGCTTCCACCTGAGAGGGACCTCTCCATGTGAGCCTCATCAGA 1320
 1261 TGGAGGATGTGCTTCCACCTGAGAGGGACCTCTCCATGTGAGCCTCATCAGA 1320
 1321 GCCTCACCTGGAGAGTGCCTGCTCTCCAGGAGCAGATCAGTGCAGTGTG 1380
 1321 GCCTCACCTGGAGAGTGCCTGCTCTCCAGGAGCAGATCAGTGCAGTGTG 1380
 1381 ACTGAAATGCTCATCACTTAAGCAACCAAGCAGTGAATGAGCTCTTCTGTTCTCTG 1440
 1381 ACTGAAATGCTCATCACTTAAGCAACCAAGCAGTGAATGAGCTCTTCTGTTCTCTG 1440
 1441 TGTCTTCTGTTTCTGTTGTAATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 1441 TGTCTTCTGTTTCTGTTGTAATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
 1501 GGGAGAAAGGCTGGGCGCCGAGTCAACAGGATGCTTGGGTGCTGCTGCTGCTGCTGCTG 1560
 1501 GGGAGAAAGGCTGGGCGCCGAGTCAACAGGATGCTTGGGTGCTGCTGCTGCTGCTGCTG 1560
 1561 CTGCGCGAGCTTTCTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1620
 1561 CTGCGCGAGCTTTCTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1620
 1621 CAGGCTGGGAGTCACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680
 1621 CAGGCTGGGAGTCACTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680
 1681 CAGCTGTGTAGAGGACAAAGAAAGTGAAGTCAACATCCGCTTCTGCTGCTGCTGCTGCT 1740
 1681 CAGCTGTGTAGAGGACAAAGAAAGTGAAGTCAACATCCGCTTCTGCTGCTGCTGCTGCT 1740
 1741 CGGGGCCCCGGGCAACAGATGAGAGATCATGTGAAGGAGTGTGCTCAGCAGGCC 1800
 1741 CGGGGCCCCGGGCAACAGATGAGAGATCATGTGAAGGAGTGTGCTCAGCAGGCC 1800
 1801 TCCTGTTTCCGCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 1801 TCCTGTTTCCGCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
 1861 CCCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
 1861 CCCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
 1921 TGAATGCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 1921 TGAATGCACTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 1981 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGGTCTTCTTCTTCTTCTTCTTCT 2040

1981 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTTCTTGGGGTCTCCTCATCCAGCCCGTCG 2040
 2041 CAGCTTTGACATCTTGTGTACTCATGTGCTTCTCTCTCTGTTTACCCCTTCCAGTATT 2100
 2041 CAGCTTTGACATCTTGTGTACTCATGTGCTTCTCTCTCTGTTTACCCCTTCCAGTATT 2100
 2101 ACCATTTGCCCTCACCTGCTTGTGTAGTGCAGCTTTTGTGCAAGACAGATGGGCTGTTT 2160
 2101 ACCATTTGCCCTCACCTGCTTGTGTAGTGCAGCTTTTGTGCAAGACAGATGGGCTGTTT 2160
 2161 TCCCCCACCCTTGAGTGTGGAGGTCAATACAGCTCTTTTATTTGCTTCTTCTTCTTCT 2220
 2161 TCCCCCACCCTTGAGTGTGGAGGTCAATACAGCTCTTTTATTTGCTTCTTCTTCTTCT 2220
 2221 GCCTCTGAATGTTTCT 2280
 2221 GCCTCTGAATGTTTCT 2280
 2281 GCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2340
 2281 GCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2340
 2341 AAAAAAAAAAAAAA 2356
 2341 AAAAAAAAAAAAAA 2356

RESULT 3
 ADP18776
 ID ADP18776 standard; cDNA; 2356 BP.
 XX ADP18776;
 XX 26-AUG-2004 (first entry)
 XX Human secreted polynucleotide #32.
 XX Human; secreted protein; gene; ss; genetic disease.
 XX Homo sapiens.
 XX US2004110939-A1.
 XX 10-JUN-2004.
 PD 15-OCT-2001; 2001US-00978360.
 XX 17-DEC-1998; 98WO-IB002122.
 PR 09-FEB-1999; 99WO-IB000282.
 PR 21-JUN-2000; 2000WO-IB000951.
 PR 15-SEP-2000; 2000US-00663600.
 XX (GEST) GENSET SA.
 PA Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
 PI Duclert A;
 XX WPI; 2004-440404/41.
 DR P-PSDB; ADP19181.
 XX New isolated polynucleotide encoding secreted polypeptide, useful for
 gene therapy, or in diagnostic procedures to identify individuals having
 genetic diseases resulting from abnormal expression of the genes.
 XX Claim 1; SEQ ID NO 32; 113pp; English.
 XX The invention relates to human cDNA sequences that encode human secreted
 proteins. The invention also relates to an antibody that specifically
 binds to a polypeptide of the invention and a method of binding the
 polypeptide to an antibody. The polynucleotides are useful for expressing
 the entire secreted proteins which they encode and for distinguishing
 human tissues and cells from non-human tissues and cells, and for
 distinguishing between human tissues and cells that do or do not express

CC the polynucleotides comprising the cDNAs. The polynucleotides and
 CC polypeptides are useful in forensic procedures or diagnostic procedures
 CC to identify individuals with genetic diseases resulting from abnormal
 CC expression of the genes corresponding to the cDNAs. The sequences are
 CC also useful in gene therapy to control or treat genetic diseases. This
 CC sequence represents a human secreted polynucleotide of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.

XX
 SQ Sequence 2356 BP; 494 A; 651 C; 665 G; 546 T; 0 U; 0 Other;

Query Match		100.0%;	Score 2356;	DB 12;	Length 2356;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2356;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATCCTTCGGCCACAGTCGGCCACCGGGCTCGCGCGCTCATCGAGAGCGGAGCGGC	60		
Db	1	ATCCTTCGGCCACAGTCGGCCACCGGGCTCGCGCGCTCATCGAGAGCGGAGCGGC	60		
Qy	61	CCTCGTGTGCAATTCATCTCTCTGGGCAACACCTGTGGTCAACCGCCCTGTACT	120		
Db	61	CCTCGTGTGCAATTCATCTCTCTGGGCAACACCTGTGGTCAACCGCCCTGTACT	120		
Qy	121	CCGTGTACCGCAGAGCCCGGGCTCTCCAGAGCTCAGGAGCTCAAGGAGCTTCAAT	180		
Db	121	CCGTGTACCGCAGAGCCCGGGCTCTCCAGAGCTCAGGAGCTCAAGGAGCTTCAAT	180		
Qy	181	TGGGTGAAGATTTAAAGATATCTTTAGAGAGCTCCAGGAAATGGGTGCTTATGCTG	240		
Db	181	TGGGTGAAGATTTAAAGATATCTTTAGAGAGCTCCAGGAAATGGGTGCTTATGCTG	240		
Qy	241	TTATAGAGGAGCTGTGCGTCTGTAAAGAAACGCTTAAACAGCAGTTGTGAAACT	300		
Db	241	TTATAGAGGAGCTGTGCGTCTGTAAAGAAACGCTTAAACAGCAGTTGTGAAACT	300		
Qy	301	GCAAGGGGTAATTCAGCGGTGACATTCAGGAGCACAGATGGTGGATCGAACCA	360		
Db	301	GCAAGGGGTAATTCAGCGGTGACATTCAGGAGCACAGATGGTGGATCGAACCA	360		
Qy	361	CCCACTTTGGAATGATTTGCTCAAGATCATTTATCAGAGGACCAACACAGTGCCTTTG	420		
Db	361	CCCACTTTGGAATGATTTGCTCAAGATCATTTATCAGAGGACCAACACAGTGCCTTTG	420		
Qy	421	ACCTGTGCCCCACAGAGATGGGTGATGTGCTGTGCGAGTGTGAGCCCTGTGACT	480		
Db	421	ACCTGTGCCCCACAGAGATGGGTGATGTGCTGTGCGAGTGTGAGCCCTGTGACT	480		
Qy	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTTCACCCCTCGATTCAGTCCCTCA	540		
Db	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTTCACCCCTCGATTCAGTCCCTCA	540		
Qy	541	CCGATGTCTCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGATCCAGAGACCGAGG	600		
Db	541	CCGATGTCTCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGATCCAGAGACCGAGG	600		
Qy	601	AGATGCTGAAGTGGGGCCACCTCAACAGGGTTGGCGAACTGGTCTGGACAACT	660		
Db	601	AGATGCTGAAGTGGGGCCACCTCAACAGGGTTGGCGAACTGGTCTGGACAACT	660		
Qy	661	CTGTCCGCTTCAGCGGCCCAACAGGATGTCAGTACTATCTAAGCAGCCAGACTTCG	720		
Db	661	CTGTCCGCTTCAGCGGCCCAACAGGATGTCAGTACTATCTAAGCAGCCAGACTTCG	720		
Qy	721	ACAGCTGTCTCAGAGGAGGAGTGTGAGCTCAGCTCTGGAAGTGTGCGGTGGTTT	780		
Db	721	ACAGCTGTCTCAGAGGAGGAGTGTGAGCTCAGCTCTGGAAGTGTGCGGTGGTTT	780		
Qy	781	TTGGCTTTGCCATGTGCCACCTCTTCTTCAATTCCTCGGAAGCAGTATCTGAGCGGC	840		
Db	781	TTGGCTTTGCCATGTGCCACCTCTTCTTCAATTCCTCGGAAGCAGTATCTGAGCGGC	840		
Qy	841	AGGAGCGCTCGGCTCAAGCAGATGTCAGGAGGAGTTCAGGAGCATGAGGCCAGCTGC	900		

Db	841	AGAGCGCCTTCGCGCTCAAGCAGATGACGAGGAGTTCAGGAGCATGAGGCCAGCTGC	900		
Qy	901	TGAGCCGAGCAAGCCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTCTGA	960		
Db	901	TGAGCCGAGCAAGCCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTCTGA	960		
Qy	961	GCAGCTTCAAGTCTCGTCTTCTTCTGAGTGTGGGACAGTTTGTCTGCAACGAGTCT	1020		
Db	961	GCAGCTTCAAGTCTCGTCTTCTTCTGAGTGTGGGACAGTTTGTCTGCAACGAGTCT	1020		
Qy	1021	ACCGCGCTTTCGAGAGCCCAAGAGTCCCTATCTGCAGACAGCGCATCACCGGGTGA	1080		
Db	1021	ACCGCGCTTTCGAGAGCCCAAGAGTCCCTATCTGCAGACAGCGCATCACCGGGTGA	1080		
Qy	1081	TACCCCTGTACACAGCTAATAGTTTGAAGCCGACAGCTTGACCTGGAAGCACCCCTG	1140		
Db	1081	TACCCCTGTACACAGCTAATAGTTTGAAGCCGACAGCTTGACCTGGAAGCACCCCTG	1140		
Qy	1141	CCCCCTTTTCAGGAGTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGGGGGTAGCTGT	1200		
Db	1141	CCCCCTTTTCAGGAGTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGGGGGTAGCTGT	1200		
Qy	1201	CACCTCCAGGTATGATTGAGGAGGAATTTGGGTAGAACTCTCCAGACCCATGCTCAA	1260		
Db	1201	CACCTCCAGGTATGATTGAGGAGGAATTTGGGTAGAACTCTCCAGACCCATGCTCAA	1260		
Qy	1261	TGGCAGGATGTCGCTTTCCACCTGAGAGGGGACCTGTGTCATGTGAGGAGCTCATAGA	1320		
Db	1261	TGGCAGGATGTCGCTTTCCACCTGAGAGGGGACCTGTGTCATGTGAGGAGCTCATAGA	1320		
Qy	1321	GCCTCACCTTGGAGGATGCGGTGGGTCTCTCCAGGAGCCAGATCAGTGCAGGTGTG	1380		
Db	1321	GCCTCACCTTGGAGGATGCGGTGGGTCTCTCCAGGAGCCAGATCAGTGCAGGTGTG	1380		
Qy	1381	ACTGAAATGCTCATCACTTAAAGCACAAAGCAGTGATCAGCAGCTCTTCTGTCTGTG	1440		
Db	1381	ACTGAAATGCTCATCACTTAAAGCACAAAGCAGTGATCAGCAGCTCTTCTGTCTGTG	1440		
Qy	1441	TGCTCTCTGTTTTTCTGTTGTAATCGTCTGCTGTGGAATTTGGTGGAGACTCAGAG	1500		
Db	1441	TGCTCTCTGTTTTTCTGTTGTAATCGTCTGCTGTGGAATTTGGTGGAGACTCAGAG	1500		
Qy	1501	GGGAGGAAAGGCTGGGCCCCGAGTACAAAGGATGCTTGGTGTGCTCGCTCGAAGAGACT	1560		
Db	1501	GGGAGGAAAGGCTGGGCCCCGAGTACAAAGGATGCTTGGTGTGCTCGCTCGAAGAGACT	1560		
Qy	1561	CTGCGCAGCTTTTCTTCTTCTTCTCATGCCCCCGGAAACAGTCTTCTTCAAGATTGT	1620		
Db	1561	CTGCGCAGCTTTTCTTCTTCTTCTCATGCCCCCGGAAACAGTCTTCTTCAAGATTGT	1620		
Qy	1621	CAGGCTGGGAGGTCACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1680		
Db	1621	CAGGCTGGGAGGTCACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1680		
Qy	1681	CAGTGTGTGTAGAGGACAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	1740		
Db	1681	CAGTGTGTGTAGAGGACAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	1740		
Qy	1741	CGGGGCCCCCGGCAACAGATTTGAAGAGAGATTCATGTGAAGGAGAGTGGTTCAGGAGCC	1800		
Db	1741	CGGGGCCCCCGGCAACAGATTTGAAGAGAGATTCATGTGAAGGAGAGTGGTTCAGGAGCC	1800		
Qy	1801	TCCTGGTTTTCGCCACTGGCCCTGATTTGAACTCTCTGCACTTTGGGAGAGCTCGGGGTGT	1860		
Db	1801	TCCTGGTTTTCGCCACTGGCCCTGATTTGAACTCTCTGCACTTTGGGAGAGCTCGGGGTGT	1860		
Qy	1861	CCCTGGTTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1920		
Db	1861	CCCTGGTTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1920		
Qy	1921	TGGATGCCACTTGGCTGTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1980		
Db	1921	TGGATGCCACTTGGCTGTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1980		

Db 1921 TGGATGCCACTGGCTAGTCTCTGGCTCCTCAGAGTCTCTTGAAGGCTGTCAAGGAA 1980
 QY 1981 AAGCAGCCGGCTGGACCTGAGCATATGCTCTTGGGCTCCTCATCAGCCCTGCG 2040
 Db 1981 AAGCAGCCGGCTGGACCTGAGCATATGCTCTTGGGCTCCTCATCAGCCCTGCG 2040
 QY 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCGTCTCTTGGTGTACCCCTCCCAAGTATT 2100
 Db 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCGTCTCTTGGTGTACCCCTCCCAAGTATT 2100
 QY 2101 ACCATTGCCCTCACCTGCCCTGGTGAGCTTTTGTGCAAGACAGATGGGCTGTTT 2160
 Db 2101 ACCATTGCCCTCACCTGCCCTGGTGAGCTTTTGTGCAAGACAGATGGGCTGTTT 2160
 QY 2161 TCCCCCAGCTCTGAGTGTGAGGTGACATACAGCTCTTTTATTTAGTCCCTTTCT 2220
 Db 2161 TCCCCCAGCTCTGAGTGTGAGGTGACATACAGCTCTTTTATTTAGTCCCTTTCT 2220
 QY 2221 GCCTCTGAATGTTATCT 2280
 Db 2221 GCCTCTGAATGTTATCT 2280
 QY 2281 GCCGACACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 Db 2281 GCCGACACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 QY 2341 AAAAAAAAAAAAAA 2356
 Db 2341 AAAAAAAAAAAAAA 2356

RESULT 4

AA012597
 ID AA012597 standard; cDNA; 2413 BP.

XX AA012597;

XX 25-SEP-2001 (first entry)

XX Human protein having hydrophobic domain encoding cDNA clone HP10649.

XX Human; hydrophobic domain; gene therapy; nutritional supplement;
 cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
 multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
 haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
 Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
 haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
 contraceptive; antiinfertility; antiinflammatory; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 CDS 115..1173

FT /*tag= a
 FT /product= "Human protein having hydrophobic domain"
 FT /note= "CDS is specifically is claimed in claim 3"

XX WO200149728-A2.

XX 12-JUL-2001.

XX 28-DEC-2000; 2000WO-JP009359.

XX 06-JAN-2000; 2000JP-00000585.

XX 06-JAN-2000; 2000JP-00000588.

XX 11-JAN-2000; 2000JP-00002299.

XX 03-FEB-2000; 2000JP-00026862.

XX 03-MAR-2000; 2000JP-00058367.

XX (PROT-) PROTEGENE INC.

XX (SAGA) SAGAMI CHEM RES CENT.

XX Kato S, Kimura T;

XX WPI; 2001-418355/44.
 DR P-FSDB; AAE06602.
 XX Human proteins with hydrophobic domains and the nucleic acids encoding
 PT them, useful for preventing diagnosing and treating e.g. cancer,
 PT Alzheimer's and inflammation.
 XX Claim 4; Page 462-465; 563pp; English.
 XX The present sequence is human protein with hydrophobic domain encoding
 CC cDNA clone HP10649. The polynucleotide and polypeptide of the invention
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The polynucleotides
 CC may be used to produce the polypeptide, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. The
 CC polynucleotides and its complementary sequences may also be used as DNA
 CC probes in diagnostic assays and also used in gene therapy. The
 CC polypeptides may also be used as antigens in the production of antibodies
 CC and in assays to identify modulators of polypeptide expression and
 CC activity. The polypeptides and nucleic acids may be used as nutritional
 CC supplements, to modulate cytokine and cell proliferation activity, to
 CC modulate immune stimulation or suppression (e.g. for the treatment of
 CC microbial infections and autoimmune disorders such as multiple sclerosis,
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's
 CC disease), to modulate active and inhibitory activity (e.g. for controlling
 CC fertility), to modulate chemotactic and chemokinetic activity, to
 CC modulate haemostatic and thrombolytic activity, to modulate receptor
 CC ligand activity, to modulate inflammation and to inhibit tumour growth
 XX
 SQ Sequence 2413 BP; 487 A; 665 C; 700 G; 561 T; 0 U; 0 Other;

Query Match 99.3%; Score 2338.4; DB 4; Length 2413;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATCCTTGGCGCCACAGTCGGCCACGGGGCTCGCGCGCTCATGGAGAGCGAGGCGCGC 60
 Db 74 ATCCTTGGCGCCACAGTCGGCCACGGGGCTCGCGCGCTCATGGAGAGCGAGGCGCGC 133
 QY 61 CCTCGCTGTGCGAGTTCATCTCTGGGCACACCTCTGTGTGTGTGTGTGTGTGTGTGTGT 120
 Db 134 CCTCGCTGTGCGAGTTCATCTCTGGGCACACCTCTGTGTGTGTGTGTGTGTGTGTGTGT 193
 QY 121 CCGTGTACCGGCAGAGCGCGCGGTCTCCCAAGAGCTCAAGGAGCTAAAAAAGTTCATT 180
 Db 194 CCGTGTACCGGCAGAGCGCGCGGTCTCCCAAGAGCTCAAGGAGCTAAAAAAGTTCATT 253
 QY 181 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGTGTG 240
 Db 254 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGTGTG 313
 QY 241 TTATAGAGGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACAGCAGTTCGTGGAAGAACT 300
 Db 314 TTATAGAGGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACAGCAGTTCGTGGAAGAACT 373
 QY 301 GCAAGGGGGTAAATTCAGCGGCTGACCTTCAGGAGCACAAGATGGTGTGGAATCGAACCA 360
 Db 374 GCAAGGGGGTAAATTCAGCGGCTGACCTTCAGGAGCACAAGATGGTGTGGAATCGAACCA 433
 QY 361 CCGACCTTTGGAATGATGTCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG 420
 Db 434 CCGACCTTTGGAATGATGTCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG 493
 QY 421 ACCTGTGTGCCCCCAGGAGTGGCGGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Db 494 ACCTGTGTGCCCCCAGGAGTGGCGGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 553
 QY 481 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTTCACACCCCTCGAGTTCAGTCTTCA 540
 Db 554 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTTCACACCCCTCGAGTTCAGTCTTCA 613

QY	1621	CAGGCTGGGAGGTCACATTGTGTTCTTTCCCTCACCCTGTGCTCTTAAACGCGTG	1681
DB	1694	CAGGCTGGGAGGTCACATTGTGTTCTTTCCCTCACCCTGTGCTCTTAAACGCGTG	1753
QY	1681	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACACATCCGCTTCTGCCAGATGGT	1740
DB	1754	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACATCCGCTTCTGCCAGATGGT	1813
QY	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGACGGCC	1800
DB	1814	TGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGACGGCC	1873
QY	1801	TCCTGGTTTTCGCCACTGGCCCTGATTTGAACTCCTCGCCACTTGGGAGAGCTCGGGTGGT	1860
DB	1874	TCCTGGTTTTCGCCACTGGCCCTGATTTGAACTCCTCGCCACTTGGGAGAGCTCGGGTGGT	1933
QY	1861	CCCTGGTTTTCCCTCTCGGAGATGAGGCGCAGAGGCTCGCCCTCTCTGAAGGACGCGATG	1920
DB	1934	CCCTGGTTTTCCCTCTCGGAGATGAGGCGCAGAGGCTCGCCCTCTCTGAAGGACGCGATG	1993
QY	1921	TGGATGCCACTGGCCTAGTGTCTCGGCTCACAGCTTCCTTGAAGGCTGTCAAGGAA	1980
DB	1994	TGGATGCCACTGGCCTAGTGTCTCGGCTCACAGCTTCCTTGAAGGCTGTCAAGGAA	2053
QY	1981	AAGCAGCGGGTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2040
DB	2054	AAGCAGCGGGTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2113
QY	2041	CAGCTTTGACATCTTGTGTACTCATGTGCTCTCTCTGTGTACCCCTCCAGTATT	2100
DB	2114	CAGCTTTGACATCTTGTGTACTCATGTGCTCTCTCTGTGTACCCCTCCAGTATT	2173
QY	2101	ACCATTTGCCCTCACCTGCCCTTGGTGAGCCCTTTAGTGCAGACAGATGGGGCTGTTT	2160
DB	2174	ACCATTTGCCCTCACCTGCCCTTGGTGAGCCCTTTAGTGCAGACAGATGGGGCTGTTT	2233
QY	2161	TCCCCCACTCTGAGTAGTTGGAGGTACATACACAGCTCTTTTATTGGCCCTTTTCT	2220
DB	2234	TCCCCCACTCTGAGTAGTTGGAGGTACATACACAGCTCTTTTATTGGCCCTTTTCT	2293
QY	2221	GCCTCTGAATGTTTCATCTCTCGTCCCTCTTTGTGAGGCGAGGAAGGGTGCCTCAGGG	2280
DB	2294	GCCTCTGAATGTTTCATCTCTCGTCCCTCTTTGTGAGGCGAGGAAGGGTGCCTCAGGG	2353
QY	2281	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC	2340
DB	2354	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAAACATGTTGCAACC	2413
RESULT 5			
ABQ91949			
ID	ABQ91949 standard; cdNA; 2401 BP.		
AC	ABQ91949;		
XX			
DT	30-SEP-2002 (first entry)		
DE	Human NF-kB activating gene SEQ ID NO 76.		
XX	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;		
KW	immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;		
KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;		
KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;		
ss.			
OS	Homo sapiens.		
OS			
XX			
PN	W020253737-A1.		
XX			
PD	11-JUL-2002.		
XX			
PF	25-DEC-2001; 2001WO-JP011389.		
XX			

PR 28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-00089912.
 PR 24-AUG-2001; 2001JP-00254018.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX
 DR WPI; 2002-583617/62.
 DR P-PSDB; ABP61461.
 XX
 XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.
 XX
 PS Claim 4; Page 352-357; 841pp; Japanese.
 XX
 CC The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers, or ischaemic
 CC infections, bone diseases, AIDS, neurodegenerative diseases or disorders
 XX
 SQ Sequence 2401 BP; 485 A; 664 C; 697 G; 555 T; 0 U; 0 Other;
 Query Match 99.2%; Score 2336.8; DB 6; Length 2401;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATCTCTGGCGCACAGTCGGCCACCGGGCTCGCGCGTCTCATGGAGAGCGAGGGCGG 60
 DB 62 ATCTCTGGCGCACAGTCGGCCACCGGGCTCGCGCGTCTCATGGAGAGCGAGGGCGG 121
 QY 61 CCTCGTGTGCCAGTTCATCTCTCTGGGACACCTCTGTGGTCAACCGCCGCTGTACT 120
 DB 122 CCTCGTGTGCCAGTTCATCTCTCTGGGACACCTCTGTGGTCAACCGCCGCTGTACT 181
 QY 121 CCGTGTACCGCAGAGCGCGGTCTCCAGAGCTCAAGGAGCTTAAAGAGTTCATT 180
 DB 182 CCGTGTACCGCAGAGCGCGGTCTCCAGAGCTCAAGGAGCTTAAAGAGTTCATT 241
 QY 181 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGTCTCCAGGAAATCGCTGTATGCTG 240
 DB 242 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGTCTCCAGGAAATCGCTGTATGCTG 301
 QY 241 TTATAGAGAGAGCTGTGGGTCTGTAAAGAAACGCTTAAAGAGTTCAGTTCGAAACT 300
 DB 302 TTATAGAGAGAGCTGTGGGTCTGTAAAGAAACGCTTAAAGAGTTCAGTTCGAAACT 361
 QY 301 GCAAGGGGTAAATCAGCGGTGACACTTCAAGAGCAAGAGTGTGGAATCGAACCA 360
 DB 362 GCAAGGGGTAAATCAGCGGTGACACTTCAAGAGCAAGAGTGTGGAATCGAACCA 421
 QY 361 CCCACCTTTTGAATGATCTCAAGATCAATTCATCAGAGGACCAACAGTGCCTTTG 420
 DB 422 CCCACCTTTTGAATGATCTCAAGATCAATTCATCAGAGGACCAACAGTGCCTTTG 481
 QY 421 ACCTGGTCCCAAGAGATGGGTGAGATGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 480
 DB 482 ACCTGGTCCCAAGAGATGGGTGAGATGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 541
 QY 481 CAGTGCATCTGGGTCTAGAGATCTGTATGAGAGTTCACCCCTCGATTAGTCTTCA 540
 DB 542 CAGTGCATCTGGGTCTAGAGATCTGTATGAGAGTTCACCCCTCGATTAGTCTTCA 601
 QY 541 CCGATGTATCGGCGACATCATCAGCGGTGAGCGGCCAAAGGATCCAAAGAGACCGAGG 600
 DB 602 CCGATGTATCGGCGACATCATCAGCGGTGAGCGGCCAAAGGATCCAAAGAGACCGAGG 661

QY 601 AGATGCTGAGGTGGGGGCCACCTCAGAGGGTTCGCGAACTGCTCTGCAACAACACT 660
 DB 662 AGATGCTGAGGTGGGGGCCACCTCAGAGGGTTCGCGAACTGCTCTGCAACAACACT 721
 QY 661 CTGTCCGCTCTGAGCGCGCCCAAAACAGGCATGAGTACTATCTAAAGCAGCAGGACTTCG 720
 DB 722 CTGTCCGCTCTGAGCGCGCCCAAAACAGGCATGAGTACTATCTAAAGCAGCAGGACTTCG 781
 QY 721 ACAGCCTCTGAGAGGAGGAGTCTGAGCCTCAGGCTCTGGAAGGTCTCTGGCGCTGTTT 780
 DB 782 ACAGCCTCTGAGAGGAGGAGTCTGAGCCTCAGGCTCTGGAAGGTCTCTGGCGCTGTTT 841
 QY 781 TTGGCTTTGCGCATGTCACCT 840
 DB 842 TTGGCTTTGCGCATGTCACCT 901
 QY 841 AGAGCGCTCTGCGCTCAAGCAGATGAGGAGGAGTTCCAGGAGCATGAGGCCAGCTGC 900
 DB 902 AGAGCGCTCTGCGCTCAAGCAGATGAGGAGGAGTTCCAGGAGCATGAGGCCAGCTGC 961
 QY 901 TGAGCCGAGCAAGCCTGAGGAGAGTCTGAGAGGAGTCTGAGAGGCTGTGTAGTGTCTGA 960
 DB 962 TGAGCCGAGCAAGCCTGAGGAGAGTCTGAGAGGAGTCTGAGAGGCTGTGTAGTGTCTGA 1021
 QY 961 GCAGCTTCAAGTCTCTGCT 1020
 DB 1022 GCAGCTTCAAGTCTCTGCT 1081
 QY 1021 ACCCGCGCTTGCAGAGCGCCCAAGAGTGCCTCTATCTGAGAGAGGAGTCAACCGGGTGA 1080
 DB 1082 ACCCGCGCTTGCAGAGCGCCCAAGAGTGCCTCTATCTGAGAGAGGAGTCAACCGGGTGA 1141
 QY 1081 TACCCCTGTACAAGCTATAGTTTGAAGCGCAGCTTGAAGTCTGAGTCTGAGAGCAGCCCTG 1140
 DB 1142 TACCCCTGTACAAGCTATAGTTTGAAGCGCAGCTTGAAGTCTGAGTCTGAGAGCAGCCCTG 1201
 QY 1141 CCCCCTTTTCAAGGATTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGTGGGGTGTAGTGT 1200
 DB 1202 CCCCCTTTTCAAGGATTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGTGGGGTGTAGTGT 1261
 QY 1201 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAAACTCTCCAGAGCCCAATGCTCCAA 1260
 DB 1262 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAAACTCTCCAGAGCCCAATGCTCCAA 1321
 QY 1261 TGGCAGGATGTGCTTTTCCACCTGAGAGGGAGCCCTGCTCCATGTGAGAGCTCATCAGA 1320
 DB 1322 TGGCAGGATGTGCTTTTCCACCTGAGAGGGAGCCCTGCTCCATGTGAGAGCTCATCAGA 1381
 QY 1321 GCCTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGGAGCAGATCAGTGGCAGTGTG 1380
 DB 1382 GCCTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGGAGCAGATCAGTGGCAGTGTG 1441
 QY 1381 ACTGAAATGCTCATCATCTTAAGCAACAAAGCAGTGTGAGAGCTCTTCTGTCTCTG 1440
 DB 1442 ACTGAAATGCTCATCATCTTAAGCAACAAAGCAGTGTGAGAGCTCTTCTGTCTCTG 1501
 QY 1441 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTCTGTTGAGTCTGTTGAGAGCTCTGAG 1500
 DB 1502 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTCTGTTGAGTCTGTTGAGAGCTCTGAG 1561
 QY 1501 GGGAGGAAAGCTGGGGCCCGAGTACAAAGGATGCTTTGGGTGTGCTCTCCGAGAGAGCT 1560
 DB 1562 GGGAGGAAAGCTGGGGCCCGAGTACAAAGGATGCTTTGGGTGTGCTCTCCGAGAGAGCT 1621
 QY 1561 CTGCGCAGCTTTTCTTTTCT 1620
 DB 1622 CTGCGCAGCTTTTCTTTTCT 1681
 QY 1621 CAGGTGGGAGGAGTCACTGTGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1680
 DB 1682 CAGGTGGGAGGAGTCACTGTGTTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1741

QY 1681 CACGTGTGTAGAGACAAAAGAGTGAAGTCAGACATCGCTTCTGCCCAGATGT 1740
 Db |||||
 QY 1742 CACGTGTGTAGAGACAAAAGAGTGAAGTCAGACATCGCTTCTGCCCAGATGT 1801
 Db |||||
 QY 1741 CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTCAGGCGGCC 1800
 Db |||||
 QY 1802 CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTCAGGCGGCC 1861
 Db |||||
 QY 1801 TCCTGGTTTCCCTCTGAGAAATGAGGCGAGAGGCTCGCTCTCTGAAGACGCAATG 1920
 Db |||||
 QY 1862 TCCTGGTTTCCCTCTGAGAAATGAGGCGAGAGGCTCGCTCTCTGAAGACGCAATG 1981
 Db |||||
 QY 1921 TGGATGCCACCTAGTGTCTGGCTCTACAGCTTCTGCAAGGCTGTCAAGGAA 1980
 Db |||||
 QY 1982 TGGATGCCACCTAGTGTCTGGCTCTACAGCTTCTGCAAGGCTGTCAAGGAA 2041
 Db |||||
 QY 1981 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCGTCG 2040
 Db |||||
 QY 2042 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCGTCG 2101
 Db |||||
 QY 2041 CAGCTTTGACATCTGTGTACTCATGTCGCTTCTCTTGTGTTACCCCTCCCAAT 2100
 Db |||||
 QY 2102 CAGCTTTGACATCTGTGTACTCATGTCGCTTCTCTTGTGTTACCCCTCCCAAT 2161
 Db |||||
 QY 2101 ACCATTTGCCCTCACCTGCCCTTGGTGGAGCTTTAGTGAAGAGATGGGCTGTT 2160
 Db |||||
 QY 2162 ACCATTTGCCCTCACCTGCCCTTGGTGGAGCTTTAGTGAAGAGATGGGCTGTT 2221
 Db |||||
 QY 2161 TCCGCCACCTCTGAGTGTGGAGTCAATACAGCTCTTTTATTTGTCCTTTTCT 2220
 Db |||||
 QY 2222 TCCGCCACCTCTGAGTGTGGAGTCAATACAGCTCTTTTATTTGTCCTTTTCT 2281
 Db |||||
 QY 2221 GCCTCTGAATGTTCAATCTCTGCTCTCTTGTGAGGAGGAGGAGGCTGCTCAGGG 2280
 Db |||||
 QY 2282 GCCTCTGAATGTTCAATCTCTGCTCTCTTGTGAGGAGGAGGAGGCTGCTCAGGG 2341
 Db |||||
 QY 2281 GCCGACACTAGTATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2340
 Db |||||
 QY 2342 GCCGACACTAGTATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC 2401

RESULT 6

ABQ91948
 ID ABQ91948 standard; cDNA; 2401 BP.
 AC ABQ91948;
 DT 30-SEP-2002 (first entry)
 XX Human NF-kB activating gene SEQ ID NO 74.
 DE Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 XX immunomodulator; cytostatic; antiinfective; osteopathic; neutropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;
 XX ss.
 OS Homo sapiens.
 XX WO200253737-A1.
 XX 11-JUL-2002.
 XX 25-DEC-2001; 2001WO-JP011389.
 XX 28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-0008912.
 PR 24-AUG-2001; 2001JP-00254018.
 XX

(ASAH) ASAH KASEI KOGYO KK.

Matsuda A, Honda G, Muramatsu S, Nagano Y;

WPI: 2002-583617/62.

P-PSDB; ABP61460.

NF-approximatelykB activating gene and expressed protein, applicable in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune diseases and cancer.

Claim 4; Page 345-349; 841pp; Japanese.

The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-kB (nuclear factor kappa B) activating effect. The protein and encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition and for treating e.g. inflammations, autoimmune diseases, cancers, infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic disorders

Sequence 2401 BP; 485 A; 665 C; 697 G; 554 T; 0 U; 0 Other;

Query Match 99.1%; Score 2335.2; DB 6; Length 2401;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	ATCCTTGGCGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGGCGGC	60
Db	62	ATCCTTGGCGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGGCGGC	121
QY	61	CCTCGCTGTGCCAGTTCATCTCTGGGACCACTCTGTGGTCAACGCGCCCTGTACT	120
Db	122	CCTCGCTGTGCCAGTTCATCTCTGGGACCACTCTGTGGTCAACGCGCCCTGTACT	181
QY	121	CCGTGTACCGCGCAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAGAGTTCATT	180
Db	182	CCGTGTACCGCGCAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAGAGTTCATT	241
QY	181	TGGGTGAAGATTTAAAGAGTATCTTTTCAAGCTCCAGGAAATGCTGCTTATCTG	240
Db	242	TGGGTGAAGATTTAAAGAGTATCTTTTCAAGCTCCAGGAAATGCTGCTTATCTG	301
QY	241	TTATAGAGGAGCTGTGCGGCTGTGTTAAAGAAACGCTTACAGCCAGTTTGTGAAACT	300
Db	302	TTATAGAGGAGCTGTGCGGCTGTGTTAAAGAAACGCTTACAGCCAGTTTGTGAAACT	361
QY	301	GCAAGGGGTAAATTCAGCGGCTGACACTTCAGGAGCACAAGATGCTGGAATCGAACCA	360
Db	362	GCAAGGGGTAAATTCAGCGGCTGACACTTCAGGAGCACAAGATGCTGGAATCGAACCA	421
QY	361	CCACCTTTGGAATGATGCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	420
Db	422	CCACCTTTGGAATGATGCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	481
QY	421	ACCTGTGCCCCCAGGAGTGGGATGCTGTGGTGTGCGAGTGTGAAGCCCTGACT	480
Db	482	ACCTGTGCCCCCAGGAGTGGGATGCTGTGGTGTGCGAGTGTGAAGCCCTGACT	541
QY	481	CAGTGTGCTGGGCTTAGAGACTGTATGAGAAGTTCCACCCCTCGATTTCAGTCCCTCA	540
Db	542	CAGTGTGCTGGGCTTAGAGACTGTATGAGAAGTTCCACCCCTCGATTTCAGTCCCTCA	601
QY	541	CCGATGTATCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGAGATCCAGAGACGAGG	600
Db	602	CCGATGTATCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGAGATCCAGAGACGAGG	661
QY	601	AGATCTGAAGTGGGGGCCACCTCAGAGGTTGGCGAACTGTCTCTGGACAACT	660
Db	662	AGATCTGAAGTGGGGGCCACCTCAGAGGTTGGCGAACTGTCTCTGGACAACT	721

661	CTGTCCGCTGCAGCGGCCAAACAAGGCATGCAGTACTATCTAAGCAGCAGGACTTCG	720
722	CTGTCCGCTGCAGCGGCCAAACAAGGCATGCAGTACTATCTAAGCAGCAGGACTTCG	781
721	ACAGCCTGCTGCAGAGCGAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTT	780
782	ACAGCCTGCTGCAGAGCGAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTT	841
781	TTGGCTTTGCCATGTGCCACCTCTTCTTCTTCTTCTCCGGAAGCAGTATCTCAGCGGC	840
842	TTGGCTTTGCCATGTGCCACCTCTTCTTCTTCTTCTCCGGAAGCAGTATCTCAGCGGC	901
841	AGGAGCGCTTGCCTCAACGAGATGCAGAGGAGTTCCAGGAGCATGAGGCCAGCTGC	900
902	AGGAGCGCTTGCCTCAACGAGATGCAGAGGAGTTCCAGGAGCATGAGGCCAGCTGC	961
901	TGAGCCGAGCCCAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTGTCTGA	960
962	TGAGCCGAGCCCAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTGTGTCTGA	1021
961	GCAGCTTCAAGTCTCTGGCTCTTCTGAGTGTGGCACGTTTGTTCCTGCAACGAGTCT	1020
1022	GCAGCTTCAAGTCTCTGGCTCTTCTGAGTGTGGCACGTTTGTTCCTGCAACGAGTCT	1081
1021	ACCGCGCTTTGCCAGAGCCCAAGAGTGCCTATCTCGACAGCGCATCACCCGGGTGA	1080
1082	ACCGCGCTTTGCCAGAGCCCAAGAGTGCCTATCTCGACAGCGCATCACCCGGGTGA	1141
1081	TACCCCTGTACAACAGCTAATAGTTTGGAGCCGACAGCTTGACCTGGAGAGCACCCCTG	1140
1142	TACCCCGCTACAACAGCTAATAGTTTGGAGCCGACAGCTTGACCTGGAGAGCACCCCTG	1201
1141	CCCCCTTTTCAGGAGATTTTATCTCGAGCCCTTTGGAGGACAGTGTGGGGGTAGCTGT	1200
1202	CCCCCTTTTCAGGAGATTTTATCTCGAGCCCTTTGGAGGACAGTGTGGGGGTAGCTGT	1261
1201	CACCTCCAGGTATGATTGAGGGAGGAATGGGTAGAAACTCTCAGACCCATGCTCCAA	1260
1262	CACCTCCAGGTATGATTGAGGGAGGAATCGGGTAGAAACTCTCCAGACCCATGCTCCAA	1321
1261	TGGCAGGATGCTGCTTTTCCACCTGAGAGGGACCTGTCCATGTGCAGCTCATCAGA	1320
1322	TGGCAGGATGCTGCTTTTCCACCTGAGAGGGACCTGTCCATGTGCAGCTCATCAGA	1381
1321	GCCTCACCTCGGAGGATGCGTGGCTCTCTCCAGGAGCCAGATCAGTGCAGTGTG	1380
1382	GCCTCACCTCGGAGGATGCGTGGCTCTCTCCAGGAGCCAGATCAGTGCAGTGTG	1441
1381	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGATCAGCAGCTCTTCTGTCTCTG	1440
1442	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGATCAGCAGCTCTTCTGTCTCTG	1501
1441	TGCTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGACTTGGTGGAGGACTCAGAG	1500
1502	TGCTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGACTTGGTGGAGGACTCAGAG	1561
1501	GGGAGGAAGGCTGGGCCCGGAGTACAACGAGATGCTTGGGTGCTGCCTCCGAAGAGACT	1560
1562	GGGAGGAAGGCTGGGCCCGGAGTACAACGAGATGCTTGGGTGCTGCCTCCGAAGAGACT	1621
1561	CTGCGCAGCTTTTCTCTTTTTTTCCTCATGCCCCCGGAAAACAGTCTTTCTCAGAAATGTT	1620
1622	CTGCGCAGCTTTTCTCTTTTTTTCCTCATGCCCCCGGAAAACAGTCTTTCTCAGAAATGTT	1681
1621	CAGGCTGGGCAGGTCAACTGTGTGTTCTTTCCCTCACCTGCTGCCTCTTAAACGCTG	1680
1682	CAGGCTGGGCAGGTCAACTGTGTGTTCTTTCCCTCACCTGCTGCCTCTTAAACGCTG	1741
1681	CACGTGTGTGTAGAGCACAAGAAAGTGAAGTCAGCATCCGCTTCTGCCAGATGGT	1740
1742	CACGTGTGTGTAGAGCACAAGAAAGTGAAGTCAGCATCCGCTTCTGCCAGATGGT	1801

Db 565 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTGAGTCCTTCA 624
QY 541 CCAGATGTCATCGGCCACTATCATCAGCGGTGAGCGGCCCAAGGATCCAAAGAGACCGAGG 600
Db 625 CCAGATGTCATCGGCCACTATCATCAGCGGTGAGCGGCCCAAGGATCCAAAGAGACCGAGG 684
QY 601 AGATGCTGAAGGTGGGGGCCACCCCTCACAGGGGTGGCGAACTGGTCTCTGGACAACAAC 660
Db 685 AGATGCTGAAGGTGGGGGCCACCCCTCACAGGGGTGGCGAACTGGTCTCTGGACAACAAC 744
QY 661 CTGTCCGCTGAGCGGCCCAAAACAGGCAATGCACTACTATCTAAGCAGCAGGACTTCG 720
Db 745 CTGTCCGCTGAGCGGCCCAAAACAGGCAATGCACTACTATCTAAGCAGCAGGACTTCG 804
QY 721 ACAGCCTGCTGAGAGCAGGAGTCAGCGTCTGAGGCTCTGGAAGGTGCTGGCGCTGGTTT 780
Db 805 ACAGCCTGCTGAGAGCAGGAGTCAGCGTCTGAGGCTCTGGAAGGTGCTGGCGCTGGTTT 864
QY 781 TTGGCTTTGCCACATGTGCGCACCTCTTCTTCTCAATTTCCGGAAGCAGTATCTCAGCGGC 840
Db 865 TTGGCTTTGCCACATGTGCGCACCTCTTCTTCTCAATTTCCGGAAGCAGTATCTCAGCGGC 924
QY 841 AGCAGCGCTGCGCCT-CAAGCAGATGCAAGGAGTTCAGGAGCATGAGGCCAGCTG 899
Db 925 AGCAGCGCTGCGCCTGCAAGCAGATGCAAGGAGTTCAGGAGCATGAGGCCAGCTG 984
QY 900 CTGAGCGCGAGCCAAAGCTGAGGACAGGAGTCTGAGAGCGCTGTGAGGAGCATGAGGCCAGCTG 959
Db 985 CTGAGCGCGAGCCAAAGCTGAGGACAGGAGTCTGAGAGCGCTGTGAGGAGCATGAGGCCAGCTG 1044
QY 960 AGCAGCTTCAAGTCTGCGCTCTTTCTGGAGTGTGGGACGTTTGTTCCTGCAACCGAGTGC 1019
Db 1045 AGCAGCTTCAAGTCTGCGCTCTTTCTGGAGTGTGGGACGTTTGTTCCTGCAACCGAGTGC 1104
QY 1020 TACCGCGCTTGCAGAGCCAAAGATGTCCTATCTGAGAGCGCATACCCGGGTG 1079
Db 1105 TACCGCGCTTGCAGAGCCAAAGATGTCCTATCTGAGAGCGCATACCCGGGTG 1164
QY 1080 ATACCCCTGTCAACAGCTAAATAGTTTGAAGCCGACAGCTTGACCTGGAGACCCCT 1139
Db 1165 ATACCCCTGTCAACAGCTAAATAGTTTGAAGCCGACAGCTTGACCTGGAGACCCCT 1224
QY 1140 GCCCCCTTTTCAAGGATTTTATCTCGAGCGCTTTGGAGGAGCAGTGTGGGGTAGCTG 1199
Db 1225 GCCCCCTTTTCAAGGATTTTATCTCGAGCGCTTTGGAGGAGCAGTGTGGGGTAGCTG 1284
QY 1200 TCACCTCCAGGTATGATGAGGAGGAATGGGTAGAACTCTCCAGACCCATGCTCCA 1259
Db 1285 TCACCTCCAGGTATGATGAGGAGGAATGGGTAGAACTCTCCAGACCCATGCTCCA 1344
QY 1260 ATGGCAGGATGCTGCTTTCCACCTGAGAGGGACCTGTCATGTGAGCGCTCATCAG 1319
Db 1345 ATGGCAGGATGCTGCTTTCCACCTGAGAGGGACCTGTCATGTGAGCGCTCATCAG 1404
QY 1320 AGCCTCACCTGGGAGGATGCGGTGGGCTCTCTCCAGAGCCAGATCAGTGGCAGTGT 1379
Db 1405 AGCCTCACCTGGGAGGATGCGGTGGGCTCTCTCCAGAGCCAGATCAGTGGCAGTGT 1464
QY 1380 GACTGAAAATGCTCATCATTTAAGACCAAGCAGATGATCAGCAGCTCTTCTGTTCT 1439
Db 1465 GACTGAAAATGCTCATCATTTAAGACCAAGCAGATGATCAGCAGCTCTTCTGTTCT 1524
QY 1440 GTGTCTCTGTTTTTTTCTGGTGAATCGTTGCTTGTGGAATTTGGTGGAGACTCAGA 1499
Db 1525 GTGTCTCTGTTTTTTTCTGGTGAATCGTTGCTTGTGGAATTTGGTGGAGACTCAGA 1584
QY 1500 GGGAGGAAAGCTGGGGCCCGAGTACAAACGATGCTTGGTGTGCTGCTCCGAAGAGAC 1559
Db 1585 GGGAGGAAAGCTGGGGCCCGAGTACAAACGATGCTTGGTGTGCTGCTCCGAAGAGAC 1644
QY 1560 TCTGCCGAGCTTTTCTTTTCTCTCATGCCCGGAAACAGTCTTTCTTCAGAAATG 1619
Db 1645 TCTGCCGAGCTTTTCTTTTCTCTCATGCCCGGAAACAGTCTTTCTTCAGAAATG 1704

QY 1620 TCAGGCTGGCAGGTCAACTTGTGTTTCCCTTCCCTCACCTGTGCTCTTAAACGCT 1679
Db 1705 TCAGGCTGGCAGGTCAACTTGTGTTTCCCTTCCCTCACCTGTGCTCTTAAACGCT 1764
QY 1680 GCAGCTGTGTGTAGAGCAAAAGAAAGTGAAGTCAAGCATCGCTTCTGCCAGATGG 1739
Db 1765 GCAGCTGTGTGTAGAGCAAAAGAAAGTGAAGTCAAGCATCGCTTCTGCCAGATGG 1824
QY 1740 TCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGTCAGGAGGC 1799
Db 1825 TCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGTCAGGAGGC 1884
QY 1800 CTCCTGGTTTGGCACTGGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGG 1859
Db 1885 CTCCTGGTTTGGCACTGGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGG 1944
QY 1860 TCCTCTGTTTCCCTCTCGAGAAATGAGGCGCAGAGGCTCGGCTCTCTGAAGACGAGT 1919
Db 1945 TCCTCTGTTTCCCTCTCGAGAAATGAGGCGCAGAGGCTCGGCTCTCTGAAGACGAGT 2004
QY 1920 GTGGATGCCACTGGCCCTAGTGTCTGGCCTCACAGCTTCTTCAAGGCTGTCAACAGGA 1979
Db 2005 GTGGATGCCACTGGCCCTAGTGTCTGGCCTCACAGCTTCTTCAAGGCTGTCAACAGGA 2064
QY 1980 AAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTC 2039
Db 2065 AAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTC 2124
QY 2040 GCAGCTTTACACATCTGGTGTACTCATGTGCTTCTCTTGTGTACCCCTCCCAAGTAT 2099
Db 2125 GCAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTTGTGTACCCCTCCCAAGTAT 2184
QY 2100 TACCATTTCGCCCTCACCTGGCCTTGGTGTACTTGTGAGCCTTTTAGTGAAGACAGATGGGCTGTT 2159
Db 2185 TACCATTTCGCCCTCACCTGGCCTTGGTGTACTTGTGAGCCTTTTAGTGAAGACAGATGGGCTGTT 2244
QY 2160 TTCGCCACCTCTGAGTAGTTGAGGTCAATACACAGCTCTTTTTTATGCCCCCTTTC 2219
Db 2245 TTCGCCACCTCTGAGTAGTTGAGGTCAATACACAGCTCTTTTTTATGCCCCCTTTC 2304
QY 2220 TGCCCTCTGAATGTTTCTATCTCTGCTCTCTTGTGAGGCGAGGAGGCTCCCTCAGG 2279
Db 2305 TGCCCTCTGAATGTTTCTATCTCTGCTCTCTTGTGAGGCGAGGAGGCTCCCTCAGG 2364
QY 2280 GGCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC 2339
Db 2365 GGCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC 2424
QY 2340 CAAAAA 2346
Db 2425 CAAAAA 2431

RESULT 9

AAS25835

ID AAS25835 standard; cDNA; 2446 BP.

XX

AC AAS25835;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human cDNA encoding a novel secreted protein, Seq ID 14.

XX

Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
antibacterial; virucide; fungicide; ophthalmological; vulnery;
secreted protein; rheumatoid arthritis; hyperproliferative disorder;
cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
cerebral ischaemia; angiogenesis; nervous system disorder;
Alzheimer's disease; infection; ocular disorder; corneal infection;
wound healing; epithelial cell proliferation; skin ageing; food additive;
preservative; antiproliferative.

PR 26-S

PA (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488783/53.

P-FSDB; AAU15648.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; SEQ ID NO 14; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed

Query Match 98.9%; Score 2330.8; DB 4; Length 2446;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2351; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 1 ATCTTTGGGCGCCAGTTCGGCCACCGGGCTCGCGCGGTCTGAGAGCGGAGCGGC 60
DB 82 ATCTTTGGGCGCCAGTTCGGCCACCGGGCTCGCGCGGTCTGAGAGCGGAGCGGC 141
QY 61 CCTCGCTGTGCGAGTTCATCTCTCTGGGACACACCTCTGTGGTTCACCGCGCCCTGACT 120
DB 142 CCTCGCTGTGCGAGTTCATCTCTCTGGGACACACCTCTGTGGTTCACCGCGCCCTGACT 201
QY 121 CCGTGTACCGGAGAGGCGCGGTCTCCAGAGCTCCAGGAAATCGTGCCTTATGCTG 240
DB 202 CCGTGTACCGGAGAGGCGCGGTCTCCAGAGCTCCAGGAGCTCAAGGAGCTAAAGATTCATT 180
QY 181 TGGGTGAAGATTAAAGAGTATCTTTTGAAGCTCCAGGAAATCGTGCCTTATGCTG 240
DB 262 TGGGTGAAGATTAAAGAGTATCTTTTGAAGCTCCAGGAAATCGTGCCTTATGCTG 321
QY 241 TTATAGAGAGCTGTGCGGTCTGTTTAAAGAACCGTTAACGCCAGTTTGGAAACT 300
DB 322 TTATAGAGAGCTGTGCGGTCTGTTTAAAGAACCGTTAACGCCAGTTTGGAAACT 381
QY 301 GCAAGGGGTAAATCAGCGGCTGACACTTCAGGAGCACAGATGGTGTGGAATCGAACCA 360
DB 382 GCAAGGGGTAAATCAGCGGCTGACACTTCAGGAGCACAGATGGTGTGGAATCGAACCA 441
QY 361 CCCACTTTTGAATGATTCTCAAGATCAITTCATCAGAGGACCAACAGTGCCTTTG 420
DB 442 CCCACTTTTGAATGATTCTCAAGATCAITTCATCAGAGGACCAACAGTGCCTTTG 501
QY 421 ACTGTGCCCCCAGAGGATGGGTGGATGTGGCTGTGCGAGTGTGAGGCCCTGGACT 480
DB 502 ACTGTGCCCCCAGAGGATGGGTGGATGTGGCTGTGCGAGTGTGAGGCCCTGGACT 561

QY 481 CAGTGGATCTGGGCTTAGAGACTGTGTATGAGAAAGTTCCACCCCTCGATTTCAGTCTTCA 540
DB 562 CAGTGGATCTGGGCTTAGAGACTGTGTATGAGAAAGTTCCACCCCTCGATTTCAGTCTTCA 621
QY 541 CCGATGTATCATCGGCCACTATCATAGCGGTGAGCGGCCCAAGGCGATCAAGAGACCGAGG 600
DB 622 CCGATGTATCATCGGCCACTATCATAGCGGTGAGCGGCCCAAGGCGATCAAGAGACCGAGG 681
QY 601 AGATGCTGAAGGTGGGGGCCACCTCTCAGGGGTTGGGAACTGGTCTGTCGACAACT 660
DB 682 AGATGCTGAAGGTGGGGGCCACCTCTCAGGGGTTGGGAACTGGTCTGTCGACAACT 741
QY 661 CTGTCGCCCTGACAGCCGCCCAAAACAAGGCATGCACTATCTAAGCAGCAGGACTTCG 720
DB 742 CTGTCGCCCTGACAGCCGCCCAAAACAAGGCATGCACTATCTAAGCAGCAGGACTTCG 801
QY 721 ACAGCCTGCTGCAGAGCAGGAGTTCGAGCGTTCAGGCTTCGGAAGGTCTGCGCTGCTTT 780
DB 802 ACAGCCTGCTGCAGAGCAGGAGTTCGAGCGTTCAGGCTTCGGAAGGTCTGCGCTGCTTT 861
QY 781 TTGGCTTTGGCACAATGTGCCACCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 840
DB 862 TTGGCTTTGGCACAATGTGCCACCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 921
QY 841 AGAGCGCCTGCGCCTCAAGCAGATGCAAGGAGGTTTCCAGGAGCATGAGGCCAGCTGC 900
DB 922 AGAGCGCCTGCGCCTCAAGCAGATGCAAGGAGGTTTCCAGGAGCATGAGGCCAGCTGC 981
QY 901 TGAGCCGAGCCAGCCCTGAGGACAGGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
DB 982 TGAGCCGAGCCAGCCCTGAGGACAGGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 1041
QY 961 GCAGCTTCAAGTCTCTGCTTCTTCTGAGTGTGGCAGCTTCTTCTTCTTCTTCTTCTTCTT 1020
DB 1042 GCAGCTTCAAGTCTCTGCTTCTTCTGAGTGTGGGACGTTTGTCTTCTGACCGAGTCT 1101
QY 1021 ACCGCGCCTTGGCAGAGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA 1080
DB 1102 ACCGCGCCTTGGCAGAGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA 1161
QY 1081 TACCCCTGTACACAGCTAATAGTTTGAAGACCGCAAGCTTGCCTTGAAGACCGCTG 1140
DB 1162 TACCCCTGTACACAGCTAATAGTTTGAAGACCGCAAGCTTGCCTTGAAGACCGCTG 1221
QY 1141 CCCCCTTTTTCAGGATTTTATCTCGAGGCTTTCGAGGAGCAGTGGTGGGGTAGCTGT 1200
DB 1222 CCCCCTTTTTCAGGATTTTATCTCGAGGCTTTCGAGGAGCAGTGGTGGGGTAGCTGT 1281
QY 1201 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAAAATCTCCAGACCCATGCCTCCAA 1260
DB 1282 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAAAATCTCCAGACCCATGCCTCCAA 1341
QY 1261 TGGCAGGATGCTGCCTTTCCACCTGAGAGGGAACCTGTCCATGTGACGCTCATCAGA 1320
DB 1342 TGGCAGGATGCTGCCTTTCCACCTGAGAGGGAACCTGTCCATGTGACGCTCATCAGA 1401
QY 1321 GCCTCACCTCCGGAGGATGCGCTGCGTCTCTCCAGGAGCAGATCAGTGGAGTGTG 1380
DB 1402 GCCTCACCTCCGGAGGATGCGCTGCGTCTCTCCAGGAGCAGATCAGTGGAGTGTG 1461
QY 1381 ACTGAAAATGCTCATCACTTAAAGCAACCAAGCCAGTGTATCAGCAGCTCTTCTGTTCCTG 1440
DB 1462 ACTGAAAATGCTCATCACTTAAAGCAACCAAGCCAGTGTATCAGCAGCTCTTCTGTTCCTG 1521
QY 1441 TGTCTTCTGTTTTTCTTCTGTTGAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
DB 1522 TGTCTTCTGTTTTTCTTCTGTTGAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1580
QY 1501 GGGAGGAAAGGCTGGGCCCCCGAGTACACCGATGATCCGATGCTGGTGGAGACTCAGAG 1560
DB 1581 GGGAGGAAAGGCTGGGCCCCCGAGTACACCGATGATCCGATGCTGGTGGAGACTCAGAG 1640

AA Human; gene; ds; neural disorder; immune system disorder; renal disorder;
 KW muscular disorder; respiratory disease; reproductive disorder;
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
 KW cardiovascular; nephrotropic; cystotic; antiallergic; thrombolytic;

XX New polypeptides and nucleic acids, useful in gene therapy for treating,
PT inhibiting or preventing e.g. neural, immune system, muscular,
PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
PT

XX New polypeptides and nucleic acids, useful in gene therapy for treating,
PT inhibiting or preventing e.g. neural, immune system, muscular,
PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
PT

PT renal disorders.

XX PS Claim 1; SEQ ID NO 14; 402pp; English.

XX CC The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders (e.g. gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX731/73-ABX741/67 represent human novel polynucleotides of the invention

XX SQ Sequence 2446 BP; 515 A; 666 C; 700 G; 562 T; 0 U; 3 Other;

Query Match 98.9%; Score 2330.8; DB 8; Length 2446;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2351; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 1 ATCTTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGCGCTCATGAGAGCGGAGCGGCGGC 60
DB 82 ATCTTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGCGCTCATGAGAGCGGAGCGGCGGC 141
QY 61 CTCTGCTGTCGAGTTTCATCTCTCTGGGACCACTCTGTGGTCAACCGCGCGCGCTGTACT 120
DB 142 CTCTGCTGTCGAGTTTCATCTCTCTGGGACCACTCTGTGGTCAACCGCGCGCGCTGTACT 201
QY 121 CCGTGACCGGACAGAGCGCGGGTCTCCAGAGCTCAAGGAGCTAAAGAGTTCAAT 180
DB 202 CCGTGACCGGACAGAGCGCGGGTCTCCAGAGCTCAAGGAGCTAAAGAGTTCAAT 261
QY 181 TGGGTGAAGATTTAAAGATTAATCTTTCAGAGCTCCAGGAAATGCTGCTATGCTG 240
DB 262 TGGGTGAAGATTTAAAGATTAATCTTTCAGAGCTCCAGGAAATGCTGCTATGCTG 321
QY 241 TTATAGAGAGCTGTGCGGTCTGTTAAAGAAACGCTTAAAGAGCTTTGTGAAAGT 300
DB 322 TTATAGAGAGCTGTGCGGTCTGTTAAAGAAACGCTTAAAGAGCTTTGTGAAAGT 381
QY 301 GCAAGGGGTAATTCAGCGCTGACACTTCAGAGCAAGATGGTGTGGAATCGAACA 360
DB 382 GCAAGGGGTAATTCAGCGCTGACACTTCAGAGCAAGATGGTGTGGAATCGAACA 441
QY 361 CCCACCTTTGGGATGATGCTCAAGATCAATTCATCAGAGGACCAACAGTGCCTTGG 420
DB 442 CCCACCTTTGGGATGATGCTCAAGATCAATTCATCAGAGGACCAACAGTGCCTTGG 501
QY 421 ACTGTGTCGCCACAGAGATGGCGTGGATGTGGCTGTGGAGTGTGAAAGCCCTTGGACT 480
DB 502 ACTGTGTCGCCACAGAGATGGCGTGGATGTGGCTGTGGAGTGTGAAAGCCCTTGGACT 561
QY 481 CAGTGGATCTGGTCTAGAGATGTGTATGAGAGTTCCACCCCTCGATTCAGTCTTCA 540
DB 562 CAGTGGATCTGGTCTAGAGATGTGTATGAGAGTTCCACCCCTCGATTCAGTCTTCA 621
QY 541 CCGATGTCAATCGGCCACTATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGAGG 600
DB 622 CCGATGTCAATCGGCCACTATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGAGG 681
QY 601 AGATGCTGAAGTGGGGGCAACCTCAGAGGGTGGCGAACTGGTCTCGGACCAACT 660
DB 682 AGATGCTGAAGTGGGGGCAACCTCAGAGGGTGGCGAACTGGTCTCGGACCAACT 741
QY 661 CTGTCCGCTCAGCGCGCCCAAGGATGAGTACTATCTAAGCAGCCAGGACTTCG 720
DB 742 CTGTCCGCTCAGCGCGCCCAAGGATGAGTACTATCTAAGCAGCCAGGACTTCG 801

QY 721 ACAGCTGCTGCGAGGCGAGGTCGAGCGTCTGGAAGTGTGCGCGCTGGTTT 780
DB 802 ACAGCTGCTGCGAGGCGAGGTCGAGCGTCTGGAAGTGTGCGCGCTGGTTT 861
QY 781 TTGCTTTGCGACATGTCGACCCCTCTCTTTCATTCCTCGGAAGCAGTATCTGACGCGC 840
DB 862 TTGCTTTGCGACATGTCGACCCCTCTCTTTCATTCCTCGGAAGCAGTATCTGACGCGC 921
QY 841 AGAGCGCTGCGCTCAAGCAGATGAGGAGGAGTTCAGAGCAGTATGAGCGCGAGTGC 900
DB 922 AGAGCGCTGCGCTCAAGCAGATGAGGAGGAGTTCAGAGCAGTATGAGCGCGAGTGC 981
QY 901 TGACCGGAGCAAGCCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
DB 982 TGACCGGAGCAAGCCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 1041
QY 961 GCAGCTTCAAGTCTGCTGCTCTTCTGAGTGTGGGACAGTTTGTCTGCAACCGAGTCT 1020
DB 1042 GCAGCTTCAAGTCTGCTGCTCTTCTGAGTGTGGGACAGTTTGTCTGCAACCGAGTCT 1101
QY 1021 ACCGCGCTTGGCCAGAGCCCAAGAGTGCCTATCTGCAGACAGCGCATCACCCGGGTGA 1080
DB 1102 ACCGCGCTTGGCCAGAGCCCAAGAGTGCCTATCTGCAGACAGCGCATCACCCGGGTGA 1161
QY 1081 TACCCCTGTACAACAGCTAATAGTTTGGAAAGCCGACAGCTTGAACCTGGAAGCACCCCTG 1140
DB 1162 TACCCCTGTACAACAGCTAATAGTTTGGAAAGCCGACAGCTTGAACCTGGAAGCACCCCTG 1221
QY 1141 CCCCTTTTTCAGGATTTTATCTCAGAGCTTTTGGAGGAGCAGTGTGGGGTGTAGTGT 1200
DB 1222 CCCCTTTTTCAGGATTTTATCTCAGAGCTTTTGGAGGAGCAGTGTGGGGTGTAGTGT 1281
QY 1201 CACCTCCAGTATGATTTAGGAGAGGAATGGGTAGAACTCTCCAGACCATCCTCCAA 1260
DB 1282 CACCTCCAGTATGATTTAGGAGAGGAATGGGTAGAACTCTCCAGACCATCCTCCAA 1341
QY 1261 TGGCAGATGCTGCTGCTTTCCACTGAGAGGGAACCTGTCTCATGTGACGCTCATCAGA 1320
DB 1342 TGGCAGATGCTGCTGCTTTCCACTGAGAGGGAACCTGTCTCATGTGACGCTCATCAGA 1401
QY 1321 GCCTCACCCTGGGAGGATGCGGTGGGCTCTCTCCAGAGGCGAGATCAGTGTGAGTGTG 1380
DB 1402 GCCTCACCCTGGGAGGATGCGGTGGGCTCTCTCTCCAGAGGCGAGATCAGTGTGAGTGTG 1461
QY 1381 ACTGAAATGCTCCTCATCATCTTAAGCACCAAGACAGTGTGAGTGTGAGTGTGAGTGTG 1440
DB 1462 ACTGAAATGCTCCTCATCATCTTAAGCACCAAGACAGTGTGAGTGTGAGTGTGAGTGTG 1521
QY 1441 TGTCTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1522 TGTCTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580
QY 1501 GGGAGAAAGGCTGGGCGCGGAGTCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
DB 1581 GGGAGAAAGGCTGGGCGCGGAGTCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1640
QY 1561 CTGCGCGAGCTTTCTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
DB 1641 CTGCGCGAGCTTTCTTTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1700
QY 1621 CAGGTGCGGAGGTCAGTGTGTTTCTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1701 CAGGTGCGGAGGTCAGTGTGTTTCTTTCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1760
QY 1681 CAGGTGCTGTAGAGCAAAAGAAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1740
DB 1761 CAGGTGCTGTAGAGCAAAAGAAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1820
QY 1741 CCGGCGCGCGGCAACAGATGAAGAGAGATCATGTGAAGGAGTGTGCTGAGGAGGCTGCTGCTGAGG 1800
DB 1821 CCGGCGCGCGGCAACAGATGAAGAGAGATCATGTGAAGGAGTGTGCTGAGGAGGCTGCTGCTGAGG 1880

[illegible]

Db	2168	TCCTGGTTTCGCCACTGGCCCTGATTGAACTCTCTGCCACTTGGAGAGCTCGGGTGGT	2227
QY	1861	CCCTGTTTTCCCTCCTCGAGAAATGAGCGCAGAGGCTCGCTCTCTGAAAGAGCGCAGTG	1920
Db	2228	CCCTGGTTTT-CTCTCGAGAAATGAGCGCAGAGGCTCGCTCTCTGAAAGAGCGCAGTG	2286
QY	1921	TGGATGCCACTGGCCTAGTCTTCCTGGCCCTCACAGCTTCCTTGCAGGCTGTCAACAGAA	1980
Db	2287	TGGATGCCACTGGCCTAGTCTTCCTGGCCCTCACAGCTTCCTTGCAGGCTGTCAACAGAA	2346
QY	1981	RAGCAGCGCGGTGGCACCTCAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCG	2040
Db	2347	AAGCAGCGCGGTGGCACCTCAGCATATGCCCTTTCGGGGTTCCTTCATCCAGCCCGTCG	2406
QY	2041	CAGCTTTTCACATCTTGGTGTAATCATGTCCCTCTCTCTGTGTACCCCTCCCGATTT	2100
Db	2407	CAGCTTTTCACATCTTGGTGGAATCAAGTCGCTCTCTCTGTGTGTACCCCTCCCGAT-T	2465
QY	2101	ACCAATTCGCCCTCACCTGCCCTTGGTGAGCCTTTTAACTGCACAGATGGGGCTGTTT	2160
Db	2466	ACCAATTCGCCCTCACCTGCCCTTGGTGAGCCTTTTAACTGCACAGATGGGGCTGTTT	2525
QY	2161	TCCCCCACCCTCGATGTAGTTGGAGGTCACTATACAGCTCTTTTTTTTATTCCTTTTCT	2220
Db	2526	TCCCCCACCCTTGTAGTGTAGTTGGAGGTCACTATACAGCTCTTTTTTTTATTCCTTTTCT	2585
QY	2221	GCCTCTGAATCTTCATCTCTCGTCCCTCTTGTGTGAGCGCAGAGGGGTGCCCTCAGGG	2280
Db	2586	GCCTTTGAATGTTCATTTTTTGTCTCTCTTGGCGAGGAGGAGGGGGCCCTCAGGG	2645
QY	2281	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACAATGTGCAACC	2340
Db	2646	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACAATGTGCAACC	2705
QY	2341	AAAAAAAAAAAAA 2352	
Db	2706	AAAAAAAAAAAAA 2717	
RESULT 12			
ABA82998			
ID	ABA82998 standard; DNA; 2377 BP.		
XX			
AC	ABA82998;		
XX			
DT	05-FEB-2002 (first entry)		
XX			
DE	Human transcription factor TRFX-25 coding sequence.		
XX			
KW	Human; transcription factor; TRFX; cell proliferative disease;		
KW	autoimmune disease; inflammation; cancer; AIDS; infection; cytostatic; anti-HIV;		
KW	developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;		
KW	neuroprotective; antiinflammatory; gene therapy; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200172777-A2.		
XX			
PD	04-OCT-2001.		
XX			
PF	13-MAR-2001; 2001WO-US008117.		
XX			
PR	13-MAR-2000; 2000US-018986P.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Hillman JL, Baughn MR, Yue H, Lal P, Lu DM, Patterson C;		
PI	Azimzai Y, Bandman O, Tang YL, Mathur P, Shah P, Au-Young J;		
PI	Reddy R;		
XX			
XX	WPI; 2001-570896/64.		
DR	P-PSDB; ABB50174.		
XX			

Fri Nov 12 12:23:28 2004

PT Novel transcription factor polypeptides, used to treat diseases
PT associated with altered activity and expression of TRFX, and to screen
PT for agents capable of modulating its activity.

XX Claim 11; Page 271; 327pp; English.

CC The present sequence is the coding sequence for a human transcription
CC factor. The transcription factor and its coding sequence are useful in
CC the diagnosis, treatment and prevention of diseases associated with
CC altered expression of the transcription factor e.g. cell proliferative,
CC autoimmune/inflammatory, neurological and developmental disorders. A
CC number of specific disorders/diseases are given in the specification,
CC including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic
CC dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
CC Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,
CC psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative
CC colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, stroke, and viral, bacterial, fungal and protozoal infections.
CC The present sequence maps to human chromosome 1

XX Sequence 2377 BP; 494 A; 652 C; 683 G; 548 T; 0 U; 0 Other;

Query Match 94.1%; Score 2217; DB 5; Length 2377;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2304; Conservative 0; Mismatches 5; Indels 44; Gaps 4;

QY	1	ATCCTTGGGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGCGGC	60
DB	68	ATCCTTGGGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGCGGC	127
QY	61	CCTCGCTGTGCCAGTTCATCCTCCTCGGACACACCTCTGTGGTACCGCGCCCTGTACT	120
DB	128	CCTCGCTGTGCCAGTTCATCCTCCTCGGACACACCTCTGTGGTACCGCGCCCTGTACT	187
QY	121	CCGTGTACCGGAGAGCGCGGTCTCCAGAGCTCAAGGAGCTAAGAAAGTTTCATT	180
DB	188	CCGTGTACCGGAGAGCGCGGTCTCCAGAGCTCAAGGAGCTAAGAAAGTTTCATT	247
QY	181	TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGCTG	240
DB	248	TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGCTG	307
QY	241	TTATAGAAGAGCTGTGCGTCTGTAAAGAAAGCTTAACAGCCAGTTTGTGAAACT	300
DB	308	TTATAGAAGAGCTGTGCGTCTGTAAAGAAAGCTTAACAGCCAGTTTGTGAAACT	367
QY	301	GCAAGGGGTAAATTCAGGGGTGACACTTCAGGAGCACAGATGCTGGAATCGAACCA	360
DB	368	GCAAGGGGTAAATTCAGGGGTGACACTTCAGGAGCACAGATGCTGGAATCGAACCA	427
QY	361	CCCACTTTGGAATGATGTCTCAAGATCATTCATCAGAGACCAACACAGTGCCTTTG	420
DB	428	CCCACTTTGGAATGATGTCTCAAGATCATTCATCAGAGACCAACACAGTGCCTTTG	487
QY	421	ACCTGGTCCCAACAGGATGGGTGTGATGTGCTGCGAGTGTGAAGCCCTTGACT	480
DB	488	ACCTGGTCCCAACAGGATGGGTGTGATGTGCTGCGAGTGTGAAGCCCTTGACT	547
QY	481	CAGTGGATCTGGGTCTAGAGCTGTGTATGAGAGTCCACCCCTCGATTTCAGTCTTCA	540
DB	548	CAGTGGATCTGGGTCTAGAGCTGTGTATGAGAGTCCACCCCTCGATTTCAGTCTTCA	607
QY	541	CCGATGTATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG	600
DB	608	CCGATGTATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG	667
QY	601	AGATGCTGAAGTGGGGGCCACCTTCAAGGGGTTGGGAACTGTCTCTGGACACAACT	660
DB	668	AGATGCTGAAGTGGGGGCCACCTTCAAGGGGTTGGGAACTGTCTCTGGACACAACT	727
QY	661	CTGTCCGCTGCAGCGGCCCAACAGGCATCGACTACTATCTAAGAGCCAGGACTTCG	720

DB	728	CTGTCCGCTGCAGCGGCCCAAAAGGCATGCTACTATCTAAGCAGCAGGACTTCG	787
QY	721	ACAGCTCTCTCAGAGGAGGAGTGCAGCTCAGCTCTGGAAGTGTCTGGCGCTGTT	780
DB	788	ACAGCTCTCTCAGAGGAGGAGTGCAGCTCAGCTCTGGAAGTGTCTGGCGCTGTT	847
QY	781	TTGGCTTTGCCACATGTGCCACCTCTTCTTCAATCTCCGGAAGCAGTATCTGCGCGC	840
DB	848	TTGGCTTTGCCACATGTGCCACCTCTTCTTCAATCTCCGGAAGCAGTATCTGCGCGC	907
QY	841	AGGAGCGCTGCGCTCAAGCAGATGTCAGGAGAGTTCAGGAGCATGAGGCCAGCTGC	900
DB	908	AGGAGCGCTGCGCTCAAGCAGATGTCAGGAGAGTTCAGGAGCATGAGGCCAGCTGC	967
QY	901	TGAGCGGAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTCTGTAGTGTCTGA	960
DB	968	TGAGCGGAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTCTGTAGTGTCTGA	1027
QY	961	GCAGCTTCAAGTCTCTGCTCTTCTGGAGTGTGGCACCTTTGTTCTGACCGAGTCT	1020
DB	1028	GCAGCTTCAAGTCTCTGCTCTTCTGGAGTGTGGCACCTTTGTTCTGACCGAGTCT	1087
QY	1021	ACGCGCCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGTGA	1080
DB	1088	ACGCGCCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGTGA	1147
QY	1081	TACCCCTGTACACAGCTAATAGTTTGAAGCGCACAGCTTCACCTGGAAGCACCCCTG	1140
DB	1148	TACCCCTGTACACAGCTAATAGTTTGAAGCGCACAGCTTCACCTGGAAGCACCCCTG	1207
QY	1141	CCCCCTTTTTCAGGGATTTTATCTCGAGGCTTTTGAAGAGCAGTGTGGGTAGTGT	1200
DB	1208	CCCCCTTTTTCAGGGATTTTATCTCGAGGCTTTTGAAGAGCAGTGTGGGTAGTGT	1267
QY	1201	CACCTCAGATATGATGAGGAGGAAATTTGGGTAGAACTCTCCAGACCATGCTCAA	1260
DB	1268	CACCTCAGATATGATGAGGAGGAAATTTGGGTAGAACTCTCCAGACCATGCTCAA	1327
QY	1261	TGSCAGAGTCTCCCTTCCACCTGAGAGGAGCCTCTCCATGTGTCAGCTCATCAGA	1320
DB	1328	TGSCAGAGTCTCCCTTCCACCTGAGAGGAGCCTCTCCATGTGTCAGCTCATCAGA	1387
QY	1321	GCCTCACCTTGGGAGATGCGGTGCGTCTCTCCAGAGCAGATCATGTCGAGTGTG	1380
DB	1388	GCCTCACCTTGGGAGATGCGGTGCGTCTCTCCAGAGCAGATCATGTCGAGTGTG	1447
QY	1381	ACTGAAATGCTCATCATCTTAAGACCAAGAGCAGTATCAGCAGCTCTCTCTCTG	1440
DB	1448	ACTGAAATGCTCATCATCTTAAGACCAAGAGCAGTATCAGCAGCTCTCTCTCTG	1507
QY	1441	TGCTCTCTGTTTCTTCTGTTGATGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTG	1500
DB	1508	TGCTCTCTGTTTCTTCTGTTGATGTTGCTTCTGCTGCTGCTGCTGCTGCTGCTG	1567
QY	1501	GGGAGGAAAGGCTGGGCGCCGAGTACAAAGGATGCTTGGGTGCTGCTCCGAGAGCT	1560
DB	1568	GGGAGGAAAGGCTGGGCGCCGAGTACAAAGGATGCTTGGGTGCTGCTCCGAGAGCT	1627
QY	1561	CTGCGCAGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1620
DB	1628	CTGCGCAGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1687
QY	1621	CAGCTGGGAGGCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1680
DB	1688	CAGCTGGGAGGCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1747
QY	1681	CACCTGTGTGTAGGAGCAAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1740
DB	1748	CACCTGTGTGTAGGAGCAAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1807
QY	1741	CGGGCCCCGGGCAACAGATGAGAGAGATCATGTGAAGGGCAGTGTGTCAGGAGGCC	1800
DB	1808	CGGGCCCCGGGCAACAGATGAGAGAGATCATGTGAAGGGCAGTGTGTCAGGAGGCC	1867

Db 661 AGCTGCTGAGCGGAGCCAGCCCTGAGGACAGGAGAGCTGAGAGCGCGCTGTGTAGTGT 720
 QY 955 GTCAGAGAGCTTCAAGTCTCGCTCTTCTGAGGTGTGGGACAGTGTCTTCTGTCACCG 1014
 Db 721 GTCAGAGAGCTTCAAGTCTCGCTCTTCTGAGGTGTGGGACAGTGTCTTCTGTCACCG 780
 QY 1015 AGTGTCTACCGCGCTTTCAGAGCGCCAGAGCCAGAGTGTGAGAGCGGAGTACACC 1074
 Db 781 AGTGTCTACCGCGCTTTCAGAGCGCCAGAGTGTGAGAGCGGAGTACACC 840
 QY 1075 GGGTGTATACCCCTGTACACAGCTATAGTTTGGAGGCGGACAGCTTGCACCTGGAAGCA 1134
 Db 841 GGGTGTATACCCCTGTACACAGCTATAGTTTGGAGGCGGACAGCTTGCACCTGGAAGCA 900
 QY 1135 CCCCTGCCCTCTTTCAGAGGATTTTATCTCGAGGCGCTTTCAGAGGCGAGTGTGGGGT 1194
 Db 901 CCCCTGCCCTCTTTCAGAGGATTTTATCTCGAGGCGCTTTCAGAGGCGAGTGTGGGGT 960
 QY 1195 AGCTGTACCTTCAGGTATGATTGAGGAGGAATTTGGGTAGAACTCTCCAGACCCATGC 1254
 Db 961 AGCTGTACCTTCAGGTATGATTGAGGAGGAATTTGGGTAGAACTCTCCAGACCCATGC 1020
 QY 1255 CTCCTATGAGGAGTGTGCTCTTCCACCTGAGAGGCGACCTGTCCATGTGCAGCCTC 1314
 Db 1021 CTCCTATGAGGAGTGTGCTCTTCCACCTGAGAGGCGACCTGTCCATGTGCAGCCTC 1080
 QY 1315 ATCAGAGCTTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGCGCCAGATCAGTGG 1374
 Db 1081 ATCAGAGCTTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGCGCCAGATCAGTGG 1140
 QY 1375 AGTGTGACTGAAATGCTCATCATCTTAAGCACCAGGAGTGTGAGGAGTGTGAGGAG 1434
 Db 1141 AGTGTGACTGAAATGCTCATCATCTTAAGCACCAGGAGTGTGAGGAGTGTGAGGAG 1200
 QY 1435 TTCTGTGCTCTGTTTCTGTTGTTTCTGTTGTTTCTGTTGTTTCTGTTGTTTCTGTTG 1494
 Db 1201 TTCTGTGCTCTGTTTCTGTTGTTTCTGTTGTTTCTGTTGTTTCTGTTGTTTCTGTTG 1260
 QY 1495 TCAGAGGGAGGAGGAGTGGGCGGCGGAGTACACGAGTGTGTTGGTGTCTTCCGAA 1554
 Db 1261 TCAGAGGGAGGAGGAGTGGGCGGCGGAGTACACGAGTGTGTTGGTGTCTTCCGAA 1320
 QY 1555 GAGACTGTGCGGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1614
 Db 1321 GAGACTGTGCGGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380
 QY 1615 AATTGTGAGGCTGGGAGGTCACCTGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTAA 1674
 Db 1381 AATTGTGAGGCTGGGAGGTCACCTGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTAA 1440
 QY 1675 CGCTGTGACGCTGTGTAGAGGACAAAGAAAGTGAAGTACAGCATCCGCTTCTGCGCA 1734
 Db 1441 CGCTGTGACGCTGTGTAGAGGACAAAGAAAGTGAAGTACAGCATCCGCTTCTGCGCA 1500
 QY 1735 GATGGTGGGCGGCGGCGGACACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTGAG 1794
 Db 1501 GATGGTGGGCGGCGGCGGACACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTGAG 1560
 QY 1795 CAGGCTCTGCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1854
 Db 1561 CAGGCTCTGCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1581
 QY 1855 GGTGTCTCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1914
 Db 1582 --TGTCTCTGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1639
 QY 1915 GCAGTGTGATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1974
 Db 1640 GCAGTGTGATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG 1699
 QY 1975 AAGGAAAGCAGCGGCTGGCAGCTTGCATATGCTTCTTGGGGCTCTCTCATCCAGC 2034

Db 1700 AAGGAAAGCAGCGGCTGGCAGCTGAGCATATGCTTGGGGCTCTCTATCCAGC 1759
 QY 2035 CCGTGGCAGCTTGTGACATCTTGGTACTCATGTGCTTCTCTCTGTTTACCCCTCC 2094
 Db 1760 CCGTGGCAGCTTGTGACATCTTGGTACTCATGTGCTTCTCTCTGTTTACCCCTCC 1819
 QY 2095 AGTATTACCATTTGGCCCTCACCTGCTTGGTGGAGCTTTTAGTGCAAGACAGATGGG 2154
 Db 1820 AGTATTACCATTTGGCCCTCACCTGCTTGGTGGAGCTTTTAGTGCAAGACAGATGGG 1879
 QY 2155 CTGTTTTCCTCCCTCTGAGTAGTGGAGTACATACACAGCTCTTTTATTGCCCC 2214
 Db 1880 CTGTTTTCCTCCCTCTGAGTAGTGGAGTACATACACAGCTCTTTTATTGCCCC 1939
 QY 2215 TTTTCTGCTCTGAATGTTTCT 2274
 Db 1940 TTTTCTGCTCTGAATGTTTCT 1999
 QY 2275 TCAGGGGCGGACACTAGTAGTATGATGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2334
 Db 2000 TCAGGGGCGGACACTAGTAGTATGATGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2059
 QY 2335 GCAACCAAAAAAAAAAAAAA 2355
 Db 2060 GCAACCAAAAAAAAAAAAAA 2080

RESULT 14
 AAS26296
 ID AAS26296 standard; cDNA; 1791 BP.
 XX
 AC AAS26296;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human cDNA encoding a novel secreted protein, Seq ID 475.
 XX
 KW Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; vulnerary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW Alzheimer's disease; angiogenesis; nervous system disorder;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 XX
 OS Homo sapiens.
 XX
 PN WO200155322-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001341.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 19-MAY-2000; 2000US-0198123P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
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PR	14-AUG-2000;	2000US-0225268P.
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PR	23-AUG-2000;	2000US-0227182P.
PR	23-AUG-2000;	2000US-0227009P.
PR	30-AUG-2000;	2000US-0228924P.
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PR	06-SEP-2000;	2000US-0230437P.
PR	06-SEP-2000;	2000US-0230438P.
PR	08-SEP-2000;	2000US-0231242P.
PR	08-SEP-2000;	2000US-0231243P.
PR	08-SEP-2000;	2000US-0231244P.
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PR	08-SEP-2000;	2000US-0231414P.
PR	08-SEP-2000;	2000US-0232080P.
PR	08-SEP-2000;	2000US-0232081P.
PR	12-SEP-2000;	2000US-0231968P.
PR	14-SEP-2000;	2000US-0232397P.
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PR	02-OCT-2000;	2000US-0236802P.
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PR	08-NOV-2000;	2000US-0246476P.
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PR	08-NOV-2000;	2000US-0246528P.
PR	08-NOV-2000;	2000US-0246532P.
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PR	08-NOV-2000;	2000US-0246610P.
PR	08-NOV-2000;	2000US-0246611P.
PR	08-NOV-2000;	2000US-0246613P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
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PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
PR	17-NOV-200	

CC and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed		Query Match 75.0%; Score 1766; DB 4; Length 1791;	
CC		Best Local Similarity 99.8%; Pred. No. 0;	
CC		Matches 1774; Conservative 5; Mismatches 1; Indels 1; Gaps 1;	
QY	576	CCCAAGGATCCCAAGAGACCGAGGAGATGCTGAAGGTGGGGCCACCCCTCACAGGGTT	635
Db	1	CCCAAGGATCCCAAGAGACCGAGGAGATGCTGAAGGTGGGGCCACCCCTCACAGGGTT	60
QY	636	GGCGAACTGGTCTGGACAACTCTGTCCGCTGCGAGCGGAGGATCGAGCGTCAAG	695
Db	61	GGCGAACTGGTCTGGACAACTCTGTCCGCTGCGAGCGGAGGATCGAGCGTCAAG	120
QY	696	TACTATCTAGCAGCGAGGATCTCGACAGCTGTGCGAGCGGAGGATCGAGCGTCAAG	755
Db	121	TACTATCTAGCAGCGAGGATCTCGACAGCTGTGCGAGCGGAGGATCGAGCGTCAAG	180
QY	756	CTCTGAAGGTGGTGGCGCTGTTTTTGGCTTTGCCACATGTGCCACCTCTTCTCAAT	815
Db	181	CTCTGAAGGTGGTGGCGCTGTTTTTGGCTTTGCCACATGTGCCACCTCTTCTCAAT	240
QY	816	CTCCGGAAGCAGTATCTGACGCGCAGAGGCGCTGCGCTCAAGCAGATGCGAGGAG	875
Db	241	CTCCGGAAGCAGTATCTGACGCGCAGAGGCGCTGCGCTCAAGCAGATGCGAGGAG	300
QY	876	TTCCAGGAGCATGAGGCGCAGCTCTGAGCGGAGCGCAAGCTGAGGACAGGAGTCTG	935
Db	301	TTCCAGGAGCATGAGGCGCAGCTCTGAGCGGAGCGCAAGCTGAGGACAGGAGTCTG	360
QY	936	AAGAGCGCCTGTGTAGTGTGTCTGAGCAGCTTCAAGTCTTCTGGAGTGTGGG	995
Db	361	AAGAGCGCCTGTGTAGTGTGTCTGAGCAGCTTCAAGTCTTCTGGAGTGTGGG	420
QY	996	CACGTTTGTCTGCAACGAGTGTACCGGCGCTTGCAGAGCCCAAGAGTGCCTTATC	1055
Db	421	CACGTTTGTCTGCAACGAGTGTACCGGCGCTTGCAGAGCCCAAGAGTGCCTTATC	480
QY	1056	TGCAGACAGCGCATCACCGGCTGATACCCCTGTACACAGCTAATAGTTTGGAGCGGC	1115
Db	481	TGCAGACAGCGCATCACCGGCTGATACCCCTGTACACAGCTAATAGTTTGGAGCGGC	540
QY	1116	ACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTCAAGGATTTTATCTCGAGGCTTTG	1175
Db	541	ACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTCAAGGATTTTATCTCGAGGCTTTG	600
QY	1176	GAGGAGCAGTGGTGGGGTACTGTCACTCAGGTATGATTGAGGAGGAAATGGGTAG	1235
Db	601	GAGGAGCAGTGGTGGGGTACTGTCACTCAGGTATGATTGAGGAGGAAATGGGTAG	660
QY	1236	AAACTCTCCAGACCATGCTCCAAATGGCAGGATGCTGCCCTTTGCCACTGAGAGGGGAC	1295
Db	661	AAACTCTCCAGACCATGCTCCAAATGGCAGGATGCTGCCCTTTGCCACTGAGAGGGGAC	720
QY	1296	CCTGTCCATGTGCAAGCTCATCAGAGCTCAACCTGGGAGGATGCCGTGGCTCTCTCC	1355
Db	721	CCTGTCCATGTGCAAGCTCATCAGAGCTCAACCTGGGAGGATGCCGTGGCTCTCTCC	780
QY	1356	CAGGAGCCAGATCAGTGGAGTGTGACTGAAATGCGCTCATCACTTAAGACCAAGGCA	1415
Db	781	CAGGAGCCAGATCAGTGGAGTGTGACTGAAATGCGCTCATCACTTAAGACCAAGGCA	840
QY	1416	GTGATCAGCAGCTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCT	1475

Db	841	GTGATCAGCAGCTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTTCT	900
QY	1476	TGTGACATTTGTTGGAGTCTCAGAGGAGGAGAAAGCTCGGCCCGAGTACAAGCATGC	1535
Db	901	TGTGACATTTGTTGGAGTCTCAGAGGAGGAGAAAGCTCGGCCCGAGTACAAGCATGC	960
QY	1536	CTTGGTGTCTGCTCCGAAGAGACTCTGCCGAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1595
Db	961	CTTGGTGTCTGCTCCGAAGAGACTCTCGCGCAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1020
QY	1596	GGAAACAGTCTTCTTCAAAATTTGTCAGGCTGGGAGGTCAACTTGTGTCTTCTTCTTCTTCTTCTTCT	1655
Db	1021	GGAAACAGTCTTCTTCAAAATTTGTCAGGCTGGGAGGTCAACTTGTGTCTTCTTCTTCTTCTTCTTCT	1080
QY	1656	CACCTGCTTGGCTTCTTAACGCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCA	1715
Db	1081	CACCTGCTTGGCTTCTTAACGCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCA	1140
QY	1716	GCACATCCGCTTCTGCCAGATGTCGGGCGCCCGGGCAACAGATTTGAAGAGAGATCATG	1775
Db	1141	GCACATCCGCTTCTGCCAGATGTCGGGCGCCCGGGCAACAGATTTGAAGAGAGATCATG	1200
QY	1776	TGAAGGCGAGTGGTTCAGGCGAGCTCTGTGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1835
Db	1201	TGAAGGCGAGTGGTTCAGGCGAGCTCTGTGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1260
QY	1836	GCCACTTGGGAGAGCTCGGGGTGCTCCCTGTTTCCCTCTCGAGAAATGAGGCGCAGAG	1895
Db	1261	GCCACTTGGGAGAGCTCGGGGTGCTCCCTGTTTCCCTCTCGAGAAATGAGGCGCAGAG	1320
QY	1896	GCCTCGCTCTCTGAAGGACGCTGTGGATGCCATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1955
Db	1321	GCCTCGCTCTCTGAAGGACGCTGTGGATGCCATTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1380
QY	1956	TTCTCTTGAAGGCTGTCAAAAGGAAAGCAGCGGCTGGCACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	2015
Db	1381	TTCTCTTGAAGGCTGTCAAAAGGAAAGCAGCGGCTGGCACTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT	1440
QY	2016	TGGGGCTCCCTCATCCAGCCCGCTTGCAGCTTTGCACATCTTGGTGTACTCATGTGCTTCT	2075
Db	1441	TGGGGCTCCCTCATCCAGCCCGCTTGCAGCTTTGCACATCTTGGTGTACTCATGTGCTTCT	1500
QY	2076	CTTGTGTATACCCCTCCCAATTTACATTTGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT	2135
Db	1501	CTTGTGTATACCCCTCCCAATTTACATTTGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT	1560
QY	2136	TAGTGAAGACAGATGGGGCTGTTTCCCGCACTCTGAGTAGTGTGAGGTCAATACAC	2195
Db	1561	TAGTGAAGACAGATGGGGCTGTTTCCCGCACTCTGAGTAGTGTGAGGTCAATACAC	1620
QY	2196	AGCTCTTCTTTTATTTGCCCTTTCTGCTCTGAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2255
Db	1621	AGCTCTTCTTTTATTTGCCCTTTCTGCTCTGAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1680
QY	2256	AGGCGAAGAGGGGTGCTTCCAGGGCGACACTAGTAGTATGATGAGTGTCCAGTGTGAAC	2315
Db	1681	AGGCGAAGAGGGGTGCTTCCAGGGCGACACTAGTAGTATGATGAGTGTCCAGTGTGAAC	2356
QY	2316	AGCAGAAATTAACATGTTGCAACCAAAAAAAAAAAAAA	2356
Db	1740	AGCAGAAATTAACATGTTGCAACCAAAAAAAAAAAAAA	1780

RESULT 15
ABX73637
ID ABX73637 standard; DNA; 1791 BP.
XX
AC ABX73637;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human novel polynucleotide #465.
XX

KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;
 KW muscular disorder; respiratory disease; reproductive disorder, disorder;
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;
 KW blood-related disorder; cancer; immunosuppressive; antiinflammatory;
 KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
 KW haemostatic; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 XX US2002132753-A1.
 XX
 PD 19-SEP-2002.
 XX
 XX
 XX 17-JAN-2001; 2001US-00764864.
 XX
 PR 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
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 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
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 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX

DR WPI; 2003-147444/14.
 DR P-PSDB; ABU55377.
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.
 XX
 PS Claim 1; SEQ ID NO 475; 402pp; English.
 XX
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders,
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
 CC human novel polynucleotides of the invention
 XX
 SQ Sequence 1791 BP; 373 A; 498 C; 494 G; 420 T; 0 U; 6 Other;

Query Match 75.0%; Score 1766; DB 8; Length 1791;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1774; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
 QY 576 CCCAAGGCATCCAAAGAGACCGAGAGATGCTGAAGTGGGGCCACCCCTCACAGGGGTT 635
 DB 1 CCCAAGGCATCCAAAGAGACCGAGAGATGCTGAAGTGGGGCCACCCCTCACAGGGGTT 60
 QY 636 GCGCACTGGTCTGGACAACAACCTCTGTCGCTCGAGCGCCCAACAGGATGCGAG 695
 DB 61 GCGCACTGGTCTGGACAACAACCTCTGTCGCTCGAGCGCCCAACAGGATGCGAG 120
 QY 696 TACTATCTAAGCAGCAGGACTTCGACAGCTGCTGAGAGGAGGAGTGCAGGCTCAGG 755
 DB 121 TACTATCTAAGCAGCAGGACTTCGACAGCTGCTGAGAGGAGGAGTGCAGGCTCAGG 180
 QY 756 CTCTGGAAGTGTGGCGCTGGTCTTTGGTCTTGGCCACATGTGCCACCTCTTCTTCATT 815
 DB 181 CTCTGGAAGTGTGGCGCTGGTCTTTGGTCTTGGCCACATGTGCCACCTCTTCTTCATT 240
 QY 816 CTCGGAGCAGTATCTGACGGGAGGAGCGCTGCGCTCAAGCAGATGCGAGGAG 875
 DB 241 CTCGGAGCAGTATCTGACGGGAGGAGCGCTGCGCTCAAGCAGATGCGAGGAG 300
 QY 876 TTCAGGAGCATGAGCCCGAGCTGTCGAGCGAGCCAGCTGAGGAGGAGTCTG 935
 DB 301 TTCAGGAGCATGAGCCCGAGCTGTCGAGCGAGCCAGCTGAGGAGGAGTCTG 360
 QY 936 AAGAGCGCTGTGTAGTGTCTGAGCAGCTTCAAGTCTGCGCTTCTTGGAGTGGG 995
 DB 361 AAGAGCGCTGTGTAGTGTCTGAGCAGCTTCAAGTCTGCGCTTCTTGGAGTGGG 420
 QY 996 CAGTTTGTCTGCAACCGAGTCTACCGCGCTTGCAGAGCCCAAGAGTCCCTATC 1055
 DB 421 CAGTTTGTCTGCAACCGAGTCTACCGCGCTTGCAGAGCCCAAGAGTCCCTATC 480
 QY 1056 TGCAGACAGCGATCACCCGGGTGATACCCCTGTACAAAGTCTGAGAGTGGAGCCGC 1115
 DB 481 TGCAGACAGCGATCACCCGGGTGATACCCCTGTACAAAGTCTGAGAGTGGAGCCGC 540
 QY 1116 ACAGCTTGACCTGGAAGACACCCCTGCGCCCTTTTTCAGGATTTTATCTCGAGGCTTTG 1175
 DB 541 ACAGCTTGACCTGGAAGACACCCCTGCGCCCTTTTTCAGGATTTTATCTCGAGGCTTTG 600
 QY 1176 GAGGAGCAGTGTGGGGGTAGTGTGTACCTCCAGGTATGATTTCAGGGAGGAATGGGTAG 1235

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1681 AGCGAGGAGGGGTG-CCTCAGGGGCCGACACTAGTATGATGAGTGTCCAGTGTGAAC 1739

2316 AGCAGAAATTAACATGTTGCAACCAAAAAA 2356
1740 AGCAGAAATTAACATGTTGCAACCAAAAAA 1780

Search completed: November 7, 2004, 22:19:56
Job time : 1060 secs

Db	601	GAGGAGCAGTGGTGGGGTAGCTGTCACTCCAGGTATGATGAGGAGAAATGGGTAG	660
Qy	1236	AAACTCTCCAGACCCATGCTCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGAC	1295
Db	661	AAACTCTCCAGACCCATGCTCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGAC	720
Qy	1296	CCTGTCCATGTGACGCTCATCAGAGCTCAACCCCTGGAGAGATGCCGTGGGTCTCTCC	1355
Db	721	CCTGTCCATGTGACGCTCATCAGAGCTCAACCCCTGGAGAGATGCCGTGGGTCTCTCC	780
Qy	1356	CAGAGCCAGATCAGTGGAGTGTGACTGAATAATGCTCATCTTAAGCACCAAGCCA	1415
Db	781	CAGAGCCAGATCAGTGGAGTGTGACTGAATAATGCTCATCTTAAGCACCAAGCCA	840
Qy	1416	GTGATCAGCAGCTCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1475
Db	841	GTGATCAGCAGCTCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	900
Qy	1476	TGTGGACTTGTGGAGGACTCAGAGGGAGGAAAGGCTGGGCCCGGAGTACAACGGATGC	1535
Db	901	TGTGGACTTGTGGAGGACTCAGAGGGAGGAAAGGCTGGGCCCGGAGTACAACGGATGC	960
Qy	1536	CTTGGGTGCTGCTCCGAGAGACTCTGCCGAGCTTTCTCTCTCTCTCTCTCTCTCTCT	1595
Db	961	CTTGGGTGCTGCTCCGAGAGACTCTGCCGAGCTTTCTCTCTCTCTCTCTCTCTCTCT	1020
Qy	1596	GGAAACAGTCTTTCTTCAAGATTGTGAGGCTGGGAGGTCAACTTGTGTCTCTTTCCCT	1655
Db	1021	GGAAACAGTCTTTCTTCAAGATTGTGAGGCTGGGAGGTCAACTTGTGTCTCTTTCCCT	1080
Qy	1656	CACCTGTCTTGCCTCTTAAACGCTGCAAGTGTGTGAGGACAAAGAAAGTGAAGTCA	1715
Db	1081	CACCTGTCTTGCCTCTTAAACGCTGCAAGTGTGTGAGGACAAAGAAAGTGAAGTCA	1140
Qy	1716	GCACATCCGCTTCTGCCAGATGCTGGGGCCCGGGCAACAGATTGAAGAGAGATCATG	1775
Db	1141	GCACATCCGCTTCTGCCAGATGCTGGGGCCCGGGCAACAGATTGAAGAGAGATCATG	1200
Qy	1776	TGAAGGGAGTGGTTCAGGAGGCTCTCTGTTTGGCCACTGGCCCTGATTTGAACTCT	1835
Db	1201	TGAAGGGAGTGGTTCAGGAGGCTCTCTGTTTGGCCACTGGCCCTGATTTGAACTCT	1260
Qy	1836	GCCACTTGGAGAGCTCGGGGTGGTCCCTGGTTTCCCTCTCTGGAGATGAGCGGAGAG	1895
Db	1261	GCCACTTGGAGAGCTCGGGGTGGTCCCTGGTTTCCCTCTCTGGAGATGAGCGGAGAG	1320
Qy	1896	GCCTCGCTTCTGAAGGAGCAGTGGATGCCACTGGCTTAGTGTCTGGCTCACAGC	1955
Db	1321	GCCTCGCTTCTGAAGGAGCAGTGGATGCCACTGGCTTAGTGTCTGGCTCACAGC	1380
Qy	1956	TTCTTTGCAAGGCTGTCAAGGAAAGCAGCGGCTGGCACCTGAGCATATGCCCTCT	2015
Db	1381	TTCTTTGCAAGGCTGTCAAGGAAAGCAGCGGCTGGCACCTGAGCATATGCCCTCT	1440
Qy	2016	TGGGGTCCCTCATCCAGCCGCTCGAGCTTTGACATCTTGTGTACTCATGTCTCTCT	2075
Db	1441	TGGGGTCCCTCATCCAGCCGCTCGAGCTTTGACATCTTGTGTACTCATGTCTCTCT	1500
Qy	2076	CCCTTGTGTACCCCTCCAGTATTACCATTTGCCCTCACCTGGCTTGGTGGGCTTT	2135
Db	1501	CCCTTGTGTACCCCTCCAGTATTACCATTTGCCCTCACCTGGCTTGGTGGGCTTT	1560
Qy	2136	TAGTGAAGACAGATGGGCTGTTTCCCCCACTCTGAGTGTGAGGTACATACAC	2195
Db	1561	TAGTGAAGACAGATGGGCTGTTTCCCCCACTCTGAGTGTGAGGTACATACAC	1620
Qy	2196	AGCTCTTTTATTGCTCTTCTGCTCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT	2255
Db	1621	AGCTCTTTTATTGCTCTTCTGCTCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCT	1680
Qy	2256	AGCGAGGAGGGGTGCCCTCAGGGGCCGACACTAGTATGATGAGTGTCCAGTGTGAAC	2315